GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

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SUMMARIES

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DEFINITION Sequence 1 from Patent W00028025.
AX024884.1 GI:10184825
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REYWORDS
SOURCE
Pholas dactylus
ORGANISM
Pholas dactylus
Pholadoidea; Pholasiactylus

ALIGNMENTS

EUKATYOTA; MeTazoa; Mollusca; Bivalvia; Hetero Pholadoidea; Pholadidae; Pholas.

AUTHORS Campbell, A.K.

TITLE Pholasin

JOURNAL Patent: WO 0028025-A 1 18-MAY-2000;

pard date

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Eukaryota; Metazoa; Mollusca; Bi
Pholadoidea; Pholadidae; Pholas.
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Pred. No. 1.8e-208;
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                           /organism="Pholas dactylus"
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Cloning and expression of the bioluminescent photoprotein
from the bivalve mollusc pholas dactylus
J. Biol. Chem. 275, 9550-9556 (2000)
Campbell, A.K.
Campbell, A.K. ő INV Dunstan, S.L., Sala-newby, G.B., Fajardo, A., Taylor, K. Length 850; 0; Indels linear /gene="phol" /function="bioluminescence photoprotein" Score 850; DB 3; Le Pred. No. 1.9e-203; mRNA /organism="Pholas dactylus" /mol_type="mRNA" /do_xref="taxon:52916" /tissue_type="photophore" /dev_stage="adult" 97.7%; Scott 100.0%; Pred. No. 100.0%; Mismatches /codon_start=1 /evidence=experimental /product="pholasin" /protein_id="CaA10291.1" /db_xref="G1:4454299" /db_xref="SPTREMBL:097465" 202 850 bp pholasin. AJJ31051.1 G1:4454298 phol gene; pholasin; photoprotein. Pholas dactylus Pholas dactylus

314 CTTCGAGGTTGGTGGAGAAATTGCCCGGCTAGTTGACTACAGACCACAGGAAGACGGAAC 373 	374 TGAGAAAACTITTACAAGAAAATICTCTAGCAAAATGCCAGGCACTTACATGCTTATGGA 433 	434 CGTGTGCGCTACAAGGGACGCTGATGATAAATGCATCGAAGGCACAATTGTGGTGACAGT 493 	494 CAGGGGGCCCTATATGACGAGGATAACAATGGTGTAATGGATGAAGGTAAGGTGATCC 553 	554 AICTGAGACAAICGAGGATGATAACAAGGACTGTGGGCTCTTAGACCAAGATGTTGAACT 613 	614 CGATTATACGTGGACTCAAAACGAGTGTGATCTACCAGACACAGTAGACGAGGCTGAAGA 673 	674 CACACCGTCAGAAACTGGAGAATTCTTCTGGTAGATCTATCAGACTACTTTTATCAGCAG 733 	734 GACAACTGGTCGTTACCAGACACCTATAACGTGTCCTCATCAATAATGTGTAAAACAGAA 793 	794 ataatcgatagaatattgaaaataabatgttaataaackctggttgaatatgaaaaaa 853 	AAAAA	04T	PDA131054 818 bp DNA linear INV 28-MAR-2000 SION AJ131054 NN AJ131054.1 GI:4454304				Direct Submission NNAL Submisted (25-NOV-1998) Campbell A.K., Medical Biochemistry, University of Wales College of Medicine, Heath Park, Cardiff, CF4 4XN, UK	RES Location/Qualifiers source 1. SI Surve Acquaism="Pholas dactylus" /mol_type="genomic DNA"	/db_xref="taxon:52916" /dev_stage="adult" gene 1 .818 /gene="phol" mRNA 1818
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QY 554 ATCTGAGACAATCGAGGATGATATCAAGGACTGTGGGCTCTTAGACCAAGATGTTGAACT 613	QY 614 CGATTATACGTGGACTCAAAACGAGTGTGATCTACCAGACACAGTGGACGAGGCTGAAGA 673	OY 674 CACACCGTCAGAAACTGGAGAATTCTTCTGGTAGATCTATCAGACTACTTTATCAGCAG 733	OY . 734 GACAACTGGTCGTTACCAGACACCTATAACGTGTCCTCATCAATAATGTGTAAAACGGAA 793 	OY 794 ATAATCGATAGAATATTGAAAATAAAATGTTAATAAACACTGGTTGAAATATGAAAAAA 853 	OY 854 AAAAA 859 Db 841 AAAAAA 846	F 4 886 WAYN 2006 WAYN 2017 WAN 2017 WAYN 2017 WAN	DEFINITION ANOMARCO 3 from Patent WO0028025. DNA 11near PAT L3-SEF-2000 DEFINITION Sequence 3 from Patent WO0028025. ACCESSION AX024886. GI:10184827	ADIROWANS Pholas dactylus SOURCE ORGANISM Pholas dactylus Bukaryoda; Metracoa; Wollusca; Bivalvia; Heteroconchia; Veneroida;	REFERENCE 1 ATTHURS Campbell, A.K.	AL Patent: V UNIV WALE S	281 a	OKLICIAN Query Watch 96.0%; Score 834.8; DB 6; Length 852; Best Local Similarity 99.2%; Pred. No. 1.3e-199; Matches 839; Conservative 0; Mismatches 7; Indels 0; Gaps 0;	CTTGTCGCTCTATGC	QY 74 GCAACCGGGTTCCGGTGGAGGAAGTACAATGCGCGATGAATTGGACAAGCTAATGAATA 133	QY 134 TGTGTTCAACGTGGACTGGATGACCATTTCATCTACGACTATGGCGCTCAAGAGCAACT 193 DD 121 TGTGTTCAACGTGGACGATTTCATCTACGACTATGGCGCTCAAGAGCAACT 180	QY 194 GTACGAAGATCGGGCTTTGGGGCTGTGTCGGATTGAACGGGCCGGCC	QY 254 AGCCGTCTGGATTAACTGGAGTAACGACGCAGTCATGTGTAACAAGAAAAACATCTT 313

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Patent: WO 0028025-A 2 18-MAY-2000;
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BDNNGVMDEGKVIPSETIEDDIKDCGLLDQDVELDYTWTQNBCDLPDTVDBAEDTPSE
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                                                       /gene="phol"
/function="bioluminescence photoprotein"
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100.0%; Pred. No. 2.2e-195;
ive 0; Mismatches 0;
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156 c 203 q
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<1. .677
 'gene="phol"
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Pred. No. 3.9e-190;
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/gene="phol"
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DEDNNGVADEGKVIPSETIEDDIKDCGLLIOQDVELDYTWTQNBCDLPDTVDEAEDTPS
                                                                                                                                                                                                                                                                                                                                                     INV 28-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cloning and expression of the bioluminescent photoprotein pholasin from the bivalve mollusc pholas dactylus
J. Biol. Chem. 275, 9550-9556 (2000)
2 (Dases 1 to 802)
Campbell.A.K.
Direct Submission
Submitted (25-NOV-1998) Campbell A.K., Medical Biochemistry, University of Wales College of Medicine, Heath Park, Cardiff, CF4
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Pholadoidea; Pholadidae; Pholas.
GTAAGGTTATTCCATCTGAGACAATCGAGGATGATATCAAGGACTGTGGGCTCTTAGACC
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                                                                                                                                                  ACGAGGCTGAAGACACACCGTCAGAAACTGGAGAATTCTTCTGGTAGATCTATCAGACTA
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                                         GTAAGGTGATTCCATCTGAGACAATCGAGGATGATATCAAGGACTGTGGGCCTCTTAGACC
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Campbell,A.K.
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/function="bioluminescence photoprotein"
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                                                                                                                                                                                                                                                                                                                                                    mRNA
clone 3.
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/mol_type="mRNA"
/db_xref="taxon:52916"
/clone="3"
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Pholas dactylus mRNA for pholasin,
AJ131052
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/dev_stage="adult"
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phol gene; pholasin; photoprotein.
Pholas dectylus
Pholas dactylus
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/db_xref="G1:4454301"
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540

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Strausberg, R. L., Feingold, E. A., Grouse, L. H., Derge, J. G.,
Strausberg, R. L., Feingold, E. A., Grouse, L. H., Shenmen, C. M., Schuler, G. D.,
Altschul, S. F., Zeeberg, B. Buetow, K. H., Schaefer, C. F., Bhat, N. K.,
Altschul, S. F., Zeeberg, B., Buetow, K. H., Schaefer, C. F., Bhat, N. K.,
Hopkins, R. F., Jordan, H., Moore, T., Mang, J. H., Mang, J. Hopkins, R. F., Cardan, H., Moore, F. A., Rubin, G. M., Hong, L.,
Stapleton, M., Soares, M. B., Bonaldo, M. F., Casavant, T. L.,
Scheetz, T. E., Brownstein, M. J., Uddin, T. B., Toshiyuki, S.
Carninci, P., Prange, C., Raha, S. S., Loquellano, M. A., Peters, G. J.,
Morley, K. C., Hale, J. M., Gunaratue, P. H., Richards, S.,
Worley, K. C., Hale, S., Garcia, A. M., Gay, L. J., Hulyk, S. W.,
Villalon, D. K., Muzny, D. M., Sodergren, E. J., Lu, X., Gibbs, R. A.,
Fahey, J., Helton, E., Ketreman, M., Madan, A., Rodriques, S.,
Bouffard, G. G., Blakesley, R. W., Touchman, J. W., Green, E. D.,
Bouffard, G. G., Blakesley, R. W., Touchman, J. W., Green, E. D.,
Butterfield, Y. S., Krzywinski, M. I., Skalska, U., Smallus, D. E.,
Schnerch, A., Schein, J. E., Jones, S. J. and Marra, M.,
Generation and initial analysis of more than 15,000 full-length
human and mouse CDM sequences.
                                                                                                                                                                                                                                                                                                                                                                                      ROD 10-JUN-2003
                                             614
                                                                                          900
                                                                                                                                        674
                                                                                                                                                                                601 GATTATACGTGGACTCAAAACGAGTGTGATCTACCAGACACAGAGACGAGGCTGAAGAC 660
                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus fascin homolog 3, actin-bundling protein, testicular (Strongylocentrotus purpuratus), mRNA (cDNA clone MGC: B8240 INAGB: 6770861), complete cds.
BC050759
BC050759
MGC.
AGGGTGTCCCTATATGACGAAGATAACAATGGTGTAATGGATGAAGGTAAGGTTATTCCA 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mushae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (09-APR-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Ghin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
                                                                          TCTGAGACAATCGAGGATGATATCAAGGACTGTGGGCCTCTTAGACCAAGATGTTGAACTC
                                                                                                                                     GATTATACGTGGACTCAAAACGAGTGTGATCTACCAGACACAGTAGACGAGGCTGAAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                         linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jopathan Kuo, NIMH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada
                                                                                                                                                                                                                              675 ACACCGTCAGAAACTGGAGAATTCTTCTGGTAGAT 709
                                                                                                                                                                                                                                                     661 ACACCGTCAGAACTGGAGAATTCTTCTGGTAGAT 695
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg, R.
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PYTDYGAQBQLYEDRALGLCKIERRGPGTYKWINNSPYDGSCYTRKTIFFEVGGEI
ARLYDYRRQAGGTEKTFTKRESKAPGTYWLADVQATRDADDKCIEGTIVYTVYSELY
DEDNNGYMDEGKYIPSETIEDDIKDCGLLDQDVELDYTWTQNECDLPDTVDEAEDFPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75 CAACCGGGTTCCGGTGAGGAAGTACAATGCGCGATGAATTGGACACAAGCTAATGAATAT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTGTTCAACGTGGACTGGATGACCATTTTCATCTACGACTATGGCGCTCAAGAGCAACTG 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TICGAGGIIGGIGGAGAAATIGCCCGGCIAGIIGACIACAGACCACAGGAAGACGGAACT 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAGAAAACTTTTACAAGAAAATTCTCTAGCAAAATGCCAGGCACTTACATGCTTATGGAC 434
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                                                                                                                                                                                                                                                                                                                                              Exeter,
UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 TCGGAAAAGAACAAAATGGCTTGTATCGTTTTCGTTGCTCTTGTCGCTCTATGCTTAATG 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TCGGAAAGGAACAAAATGGCTTGTATCGTTTTCGTTGCTCTTGTCGCTCTAGTGCTTAATG 60
                                                                     Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroida;
Pholadoidea; Pholadidae; Pholas.
1 (bases 1 to 695)
Harwood, L. J., Bryant, J. A., Littlechild, J. A., Knight, R. and
                                                                                                                                                                                   Molecular cloning of the cDNA encoding the bioluminescent protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCCGTCTGGATTAACTGGAGTAACGACACGCAGTCATGTGTAACAAGAAAAAAATCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                Knight,J.
Direct Submission
Submitted (02-APR-2002) Biological Sciences, University of I
Submitted (02-APR-2002) Biological Sciences, University of I
Washington Singer Labs, Perry Road, Exeter, Devon EX4 4QG, I
Location/Qualifiers
1. 695
                                                                                                                                                                                                                                                     2 (bases 1 to 695)
Harwood, L.J., Bryant, J.A., Littlechild, J.A., Knight, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
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Pred. No. 5.9e-162;
0; Mismatches 6; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                164 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="pholasin"
/protein_id="AAM18085.1"
/db_xref="GI:20269883"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:52916"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                188 g
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Anotes Canning Low Company (Homo sapiens) Original Length of seq 1: 3.673778 <2235-split as sapiens) Original Length of seq 1: 3.673778 <2235-split as follows:-seq 01 0.0000.001 TO 0.349.980-seq 02 0.300.001 1.249.980-seq 02 0.300.001 1.249.980-seq 06 1.500.001 1.549.980-seq 06 1.500.001 2.449.980-seq 07 1.800.001 2.749.980-seq 06 1.500.001 3.449.980-seq 10 2.700.001 3.449.980-seq 11 3.000.001 3.349.980-seq 12 3.000.001 3.449.980-seq 13 3.000.001 3.349.980-seq 14 0.000.001 TO 0.349.980-seq 15 0.300.001 649.980-seq 16 0.000.001 TO 0.349.980-seq 15 0.300.001 649.980-seq 18 1.200.001 1.549.980-seq 21 2.100.001 1.849.980-seq 20 1.800.001 2.449.980-seq 21 2.100.001 2.449.980-seq 22 2.400.001 3.349.980-seq 22 3.300.001 3.049.980-seq 22 3.300.001 3.349.980-seq 26 3.500.001 3.349.980-seq 26 3.500.001 3.349.980-seq 26 3.500.001 3.349.980-seq 26 3.500.001 3.349.980-seq 26 3.500.001
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Pred. No. 0.05;
0; Mismatches 82; Indels 0;
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Dorner,F., Scheifilinger,F. and Falkner,F.Gunter.
Recombinant fowlpox virus
Patent: US 5670367-A 14 23-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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166494
166494.1 GI:2724471
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1491 c 1486 g
                Location/Qualifiers
1. .349980
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Best Local Similarity 55.2%;
Matches 101; Conservative (
    Epigenomics AG
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                                                                                                        Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at: http://image.llnl.gov Series: IRAL Plate: 46 Row: f Column: 16 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9624991. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SVIYDAEVCAASERITQMSLEQYECDSETPTIQLRSANGYYLAQRRHRAIIADGHPME
SDTFFRUHNNCGKITLQSPNGREIGIASDGILMANYTIPGPNEELGIRFANRPFLVLR
GRYGYVGSSSDHDLLKCNMDQPDCIQLLPCRQGIYHFQAQGGSFWSITSFGFFRPWGK
FALNFCIELGGSSTLAPNGFYLRADRSGTLLADSEEITKECIWEF"
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/translation="magvDWIHRHPKAEDLRVGLISWAGTYLTFEAYKSSVTASAKSL
GRRQTWELLYSNEHESQAVIRLKSLQGLYLLCEADGTVCTGRPRTSHHGCFLLRFHRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GKWTLOCIISGRYLESDGEDVFCNSRVLSAYHMWTPRPALHVHVILYSPIYHSYARAD
HTVGRIWVDAAIPCLEEGGGFLLHFQDGGYHLETSTHHFLSRVDRLVPQRSSGYAFHMQ
VRPRGLVALCDGEGGTLYPQGSHLLLGMGSAPMKGEEWFVLQHFPTWYSLKSKSRRFL
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Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smalius, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranda Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
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Pred. No. 0.018;
0; Mismatches 72; Indels 0;
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                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/mol_type="mRNA"
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/lab_host="pullob"
/note="Vector: pDNR-LIB"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="Fscn3"
/db_xref="LocusID:56223"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="fascin 3"
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/db_xref="G1:29748039"
                                                                                                                                                                                                                                                                      /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
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                                                                                INV 29-JAN-2003
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vsvdgggilesaliergilesgildsgsvnknnmslrlnsknvm.grngeennkkkkk
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ED IENFRNTFNKEYLKSVLTNDNNNDGINNNDDNNDDNNDDNNDNNNNNNNNKNNKNS
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MANNEKGELLYGKGONNNNNNNNNSGTYVKNKKSSKYDNKSYGGDGIPRKERS
KNIVEDNIKNMNVENIKNIKDIKNVNNMNNMNMNMNNYNFLFADKKNKNNNLNIG
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                                                                                                                                                  471
                                                                                                                                                                                              352 ACAGACCACAGGAAGACGGAACTGAGAAAACTTTTACAAGAAAATTCTCTAGCAAAATGC 411
                                                                                                                                                                                                                                          472 AAGGCACAATTGTGGTGACAGTCAGGGTGTCCCTATATGACGAAGATAACAATGGTGTAA 531
                                                                                                                                                                                                                                                                                                                                             532 TGGATGAAGGTAAGGTGATTCCATCTGAGACAATCGAGGATGATATCAAGGACTGTGGGC 591
                                                                                                                                                                                                                                                                                                                                                                                                                                              592 TCTTAGACCAAGAIGTTGAACTCGATTATACGTGGACTCAAAACGAGTGTGATCTACCAG 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hall, N., Bowman, S., Churcher, C., Quail, M. and Barrell, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The Sanger Centre, Wellcome Trust Canone Campus, Hinxton, Cambrical 15A, UK
On Oct 3, 2002 this sequence version replaced gi:5731932.
For more information about this sequence or the Malaria Project, see http://www.sanger.ac.uk/Projects/P_falciparum.
Location/Qualifiers
                                                                                                                                               412 CAGGCACTTACATGCTTATGGACGTGTGCGCTACAAGGGACGCTGATGAATGCATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium. (bases 1 to 272698)
Hamilin, N., Pain,A., Berriman,B., Hall,N., Bowman,S., Churche Harnis,B., Haris,D., Lawson,D., Quail,M. and Barrell,B. Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              652 ACACAGTAGACGAGGCTGAAGACACACGGTCAGAAACTGGAG 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="plasmodium falciparum 3D7"
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/isolate="3D7"
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Plasmodium falciparum WAL4P4.
AL035477 AL844503
AL035477.6 GI:23498269
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/clone="MAL4P4"
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PFMAL4P4/c
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ORGANISM
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CDS

FEATURES

COMMENT

/gene="rbuosco."
/note="synonym: VAR"
complement(ioln(8056. 9360,9747. 14900))
/gene="PEDD0955c"
/gene="PEDD0955c"
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/note="Similar to Plasmodium falciparum variant-specific /protein_id="CAD49242.1"
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123396 AAATTTTTTTTTTTTTTTCTCCCCCTTTTAATTATATATGAATAATTTTAGG 123337
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ECNKSKVKGNEGNSEGACAPYRRLHVCDQNLELIKPKNITTHNLLVDVCLAAKFEAES
LKTYRGKYQLTNHGFHTNICTELARSFADIGDIIRGKDLYRGNNKEKDRLEDNLKKIP
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surface protein var-2 SWALL:Q26033 (EMBL:L40609) (2664 aa)
fasta scores: E(): 4.8e-101, 40.92% id in 2793 aa"
                                                                                                                                                                                           /translation="MYARGGHQGGEDIDETSAKHLLDSIGEKVYKKVHGAALQRSNGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   594 ITAGACCAAGATGTTGAACTCGATTATACGTGGACTCAAAACGAGTGTGATCTACCAGAC 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         654 ACAGTAGACGAGGCTGAAGACACACGGTCAGAAACTGGAGAATTCTTCTGGTAGATCTAT 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  714 CAGACTACTTTTATCAGCAGGACAACTGGTCGTTACCAGACACCTATAACGTGTCCTCAT 773
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     752 GACACCTATAACGTGTCCTCATCAATAATGTGTAAAAACAGAAATAATCGATAGAATATTG 811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            692 AGANTTCTTGGTAGATCTATCAGACTACTTTTATCAGCAGGACAACTGGTCGTTACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genomic DNA (Homo sapiens)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="erythrocyte membrane protein 1 (PfEMP1)"
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/db_xref="G1:23498274"
                                                                                                                                                                                                                                                                                                                                               5.5%; Score 48.2; DB 3; Length 272698; 54.9%; Pred. No. 0.39; Live 0; Mismatches 78; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Diagnosis of diseases associated with the immune system Patent: Wo 0200928-A 400 03-JAN-2002;
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Pred. No. 0.47;
0; Mismatches 141; Indels
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/mol_type="qenomic DNR"

/db_xref="taxon:32630"

/note="chemically treated genomic

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Sequence 400 from Patent WO0200928.
AX345329
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                                                                        /codon_start=1
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YHKEVENAGGLCILENNDGKEKVNKQKTYNDFFYYWVAHMLKDSIHWKKKLEKCLKNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HKKYHYDSVRLKDDDDQSGDKLQSTSAPSDTPTLNNPKLSDFVLRPTYFRYLEEWGES
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YKRWIEKKLEEFQKQKDKYKGELDKLTKDKSGGDKKFCEEIKNHSSAANFLKELKHGK
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GETWEKVFDKLAKNNGKTTTIDVHMIDRRAPFIKKYLENSKNSEBSNNSLFKDSYLLFK
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KANKCKEDQKFNGENQAQTCEKSAPVEDEDDEPLEERNPYTQPNICPKVETTEETVDE
                                                                                                                                                                                                                            LHNGEEVTYN INFDYSKNINEITNTTDDSKIYSNNIYSGIDLINDSLNSDQHVDIYDE
LLKRKENEIFOTNHTKHTTTNSIAKQTHTDPILNQLDLPHKWLDRHRNMCEQWNKNKK
EELLDKLKEEMNKKNNNNSDLTHTSSNIPSGENSIKNYLNTDYSIQIDMDDPKPINEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GELEGKLSLATTIGELNYTKDPCIFDYSKLINGSGSGGVTARDPCGNGSGKGEDYSR
FSDKEGAQCANSKIHGNSKGSNGGACAPLRRLHLCNKNMEKIATSTAKHDLLVDVCMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EENLRKIFENIYEGLSNNGVKARYEGDKENFYQLREDWWALNRDQVWKALTCSDDLKD
ASYPRPTCSDRKGSCSQAKDNCRCDGSNTDQVPTYFDYVPQFLRWFEEWAEDFCRKKK
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LCGMKKNNNGEWEHKKKGKCTSGNLYRPIDGAIHTDINFLYSGDRHDDIEKKLNRFCD
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CQQKQNECPKKPPKKTPGGPDRALKPEEVDASSEDHYDEBGGEDEEEEDKEEEGEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EDVQDDVAEEDTAKEEGSSTTETQLPDACNIVKTLFESTKNFEDACRQKYGPKAPTSW
KCVPTTGDKDGATGKSDGSICVPPRRRRLYIHKVDDNVKDDASLRKWFIESSAVETFF
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RNAPSIWKGMICALIYKEDGEKSTDDKTTLKRNDDVTEKIFGKPPNNDNPQNPNNGTF
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KSSVRNLFQILQIPKGDYDIPTKLSPNRYIPYTSGKYRGKRYIYLEGDSGTDSGYTDH
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RSNPNLMGNQNPNLNLVENNINPNHQNQNQYGDTNFVDTPTNPTNVQIEMDVNTKLVK
                                                                                                                                                                                                 WNQLKQDFISNTLQSTQMDLPNENIIDDFMDKGIQPNNPVLDVNMAEKPFITSIHDRD
                                                                                                                                                                                                                                                                                                                        IYMDNIIDNLEKNSEPYYDIDEDDIIYFDIDDEKTPMYHNNMDNNKSNVPTKVQIEMN
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                                                                     PKFCPEIPQPEPEPEPEEDTEQEEKEEKLPAAPDNSEQEETSKEVVPEKKMPTPPP
                                                                                                  KKPEQGPKQRKKQKRQLPTHTS1LPEMLS1SSFPLTVGVAFAALSYF1LKKKSKST1D
                                                                                                                                                                 TSSESEYEDIDINNIYPYKSPKYKTLIDVVLEPSKRDTFNTQSDIPSDTSTNKFTDNE
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SWALL:096296 (EMBL:AE001434) (2197 aa) fasta scores: E():
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="erythrocyte membrane protein 1 (PfEMP1)"
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RESULT 14 AEN508686/c

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DEFINITION

ACCESSION

VERSION KEYWORDS

ORGANISM

AUTHORS TITLE

REFERENCE

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Direct Submission
Submitted (20-SEP-2002) Jiggins F.M., Department of Genetics,
University of Cambridge, Downing Street, Cambridge, CB2 3EH, UNITED
KINGDOM
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LVTAGVYLLIRFNSLLVDLFFLKFLLLFSGLTMAMAGISANY EFDLKKITALSTLSQL
GLAMSILSMGFYDLAFFHLLFHAMFKALLFMCAGVIIHMANDNQDIRAMGGISLYIPL
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LNESQKLFKNIDLGWSEYKSGQGIYSIVKDNSVYYYYQMNBKIYIFESFILWVLFMI
MLILI"
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LMYLMYNDFNLYVIYNLYDEDYYMLKSMMILLAMSLISGSFISWMIFYYPYMIYLPFS
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                                                                          789 CAGAAATAATCGATAGAATATTGAAAATAAAATGTTAATAAACACTGGTTGAAATATGAA 848
Jiggins, F.M. Male-Killing Wolbachia and Mitochondrial DNA. Selective sweeps, hybrid introgression and parasite population dynamics Genetics 164 (1), 5-12 (2003)
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Male-killing Wolbachia and mitochondrial DNA: selective sweeps,
hybrid introgression and parasite population dynamics
Genetics
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Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Papilionoidea; Nymphalidae; Heliconiinae; Acraea.
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NADH dehydrogenase subunit 5; ND5 gene.
mitochondrion Acraea encedana (Pierre's acraea)
Acraea encedana
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MTILLDWASLLFMAFVSLISSSVIYYSKSYMSSELNINRFIYLVLMFVFSMALLIISP
NMISILLGWDGLGLVSYCLVIYYQNIKSYNAGMLTALSNRIGDVMILILISWALNYGS
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LVTAGVYLLIRFNSLLVDLFFLKFLILLFSGLFWMAGISANYEFDLKKIIALSTLSQL
GLMMSILSMGFYDLAFFHLLTHAMFKALLFWCAGVI IHMMIDNQDIRAMGGISLYIPL
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Submitted (20-SEP-2002) Jiggins F.M., Department of Genetics,
University of Cambridge, Downing Street, Cambridge, CB2 3EH, UNITED
KINDDOM
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gene for NADH
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Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Papilionoidea; Nymphalidae; Heliconiinae; Acraea.
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Pred. No. 0.58;
0; Mismatches 57; Indels 0
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AJ508686.1 GI:23337118
NADM dehydrogenase subunit 5; ND5 gene.
mitochondrion Acraea encedon (white-barred acraea)
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Best Local Similarity 58.7%;
Matches 81; Conservative
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BASE COUNT ORIGIN

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729 AGCAGGACAACTGGTCGTTACCAGACACCTATAACGTGTCCTCATCAATAATGTGTAAAA 788
                                                                                                                  Query Match 5.4%; Score 46.8; DB 3; Length 1716; Best Local Similarity 58.7%; Pred. No. 0.58; Matches 81; Conservative 0; Mismatches 57; Indels 0;
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(UYWA-) UNIV WALES COLLEGE OF MEDICINE,

98GB-0024357.

07-NOV-1998;

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834.8 818 799.2 725 47.4 47

Perfect score:

Sequence:

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Scoring table:

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Bivalve mollusc; apopholasin; bioluminescent oxidative indicator protein; BOIP; light emission; pholasin; oxygen; chemiluminesce; cancer cell; hyperactive cell; rheumatoid arthritis; inflammatory disease; ss.
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ABX46522
ABQ54553
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ACC50854
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Pholas dactylus.
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  CDNA sequence from CDNA sequence from CDNA sequence from CDNA sequence from PCR amplified geno Human immune syste Human cDNA SEQ ID Human polynucleoti
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                    GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Database

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GTAAGGTGATTCCATCTGAGACAATCGAGGATGATATCAAGGACTGTGGGCTCTTAGACC
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                                                                                                                                                                                                               The present sequence encodes a bivalve mollusc apopholasin protein.

The protein is a bioluminescent oxidative indicator protein (BOIP).

Changes in light emission of pholasin enable oxygen or its metabolites

to be detected and quantified in live cells, organelles or on the outer

or partism without the need to break them open or the need to separate or a timer surface of the plasma membrane, or within an organ of a live or inner surface of the plasma membrane, or within an organ of a live or inner surface of the need to break them open or the need to separate or or one of its metabolites. This also enables an enzyme producing oxygen or one of its metabolites to be detected and quantified. The BOIP includes a signal peptide whose target is set to a predetermined extra or intracellular site. The light emission preferably takes place in the nate of the luciferase. Pholasin is also useful as a protein or a DNA label or in genetic entertainment which involves adding pholasin to drink such as beer, cola, soft drinks and spirits to make them glow since compassin is able to chemiluminesce at a wide range of pH (3-10). It can also be added to foodstuffs and in a wide range of toys and other entertaining devices. BOIP nucleic acids can be used for detection and closumential arthritis and other inflammatory diseases, cells infected with content of amanged cells, and measurement and location of enzymes.
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                                                                                           Novel recombinant nucleic acid molecules that encode the apophoprotein of pholasin or its homologous sequence useful for detecting location and measurement of oxygen and its metabolites in living cells and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GAATTCGGCACGAGTCGGAAAAGAACAAATGGCTTGTATCGTTTTCGTTGCTTGTCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGGAAGACGGAACTGAGAAAACTTTTACAAGAAAATTCTCTAGCAAAATGCCAGGCACTT
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                                                                                                                                                                                       Claim 3; Fig 1; 49pp; English.
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Matches 870; Conservative
                                          WPI; 2000-387420/33.
                                                          P-PSDB; AAY93251
       Campbell AK;
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Bivalve mollusc; apopholasin; bioluminescent oxidative indicator protein; BOIP; light emission; pholasin; oxygen; chemiluminesce; cancer cell; hyperactive cell; rheumatoid arthritis; inflammatory disease; ss.
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999
                                                                                                                      661 ACGAGGCTGAAGACACACCGTCAGAAACTGGAGAATTCTTCTGGTAGATCTATCAGACTA 720
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                                                                                                                                                                                                                                                                          AAGAIGITGAACICGAITATACGIGGACICAAAACGAGIGIGATCIACCAGACACAGTAG
                                                                                                                                                                                                                                             721 CTTTTATCAGCAGGACAACTGGTCGTTACCAGACACCTATAACGTGTCCTCATCAATAAT
                                                                                                                                                                                                                                                                                                                                                                   present sequence encodes a bivalve mollusc apopholasin protein. protein is a bioluminescent oxidative indicator protein (BOIP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA sequence from clone 5 encoding apopholasin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   841 AATATGAAAAAAAAAAAAAAAAAAAAACTCGAG 870
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c changes in light emission of pholasin enable oxygen or its metabolites

to be detected and quantified in live cells, organelles or on the outer

or inner surface of the plasma membrane, or within an organ of a live

organism without the need to break them open or the need to separate

bound and free fractions. This also enables an enayme producing oxygen

or one of its metabolites to be detected and quantified. The BOIP

is used for the detection, diagnosis or measurement of oxygen or its

metabolites intracellularly or extracellularly. The BOIP includes a

signal peptide whose target is set to a predetermined extra or

intracellular site. The light emission preferenbly takes place in the

intracellular site. The light emission preferenbly takes place in the

cintracellular site. The light emission preferenbly takes place in the

six and a peptide whose target is set to a predetermined extra or

intracellular site. The light emission preferenbly takes place in the

cintracellular site of an allow since of the luciferase. Pholasin is also useful as a protein or a DNA

label or in genetic entertainment which involves adding pholasin to drink

such as beer, ocla, soft drinks and spirits to make them glow since

bolasin is able to chemiluminesce at a wide range of pH (3-10). It can

also be added to foodstuffs and in a wide range of toys and other

coloration of abnormal cells such as cancer cells, hyperactive cells in

continuous damaged cells, and measurement and location of enzymes.
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Sequence 852 BP; 281 A; 161 C; 209 G; 201 T; 0 other;

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                                                                                         74 GCAACCGGGTTCCGGTGAGGAAGTACAATGCGCGATGAATTGGACACAAGCTAATGAATA 133
                                                                                                                                      134 TGTGTTCAACGTGGACTGGATGACCATTTTCATCTACGACTATGGCGCTCAAGAGCAACT 193
                                                                                                                                                                                  CTTCGAGGTTGGTGGAGAAATTGCCCGGCTAGTTGACTACAGGACCACAGGAAGACGGAAC 373
                                                                                                                                                                                                                                                                                                                       TGAGAAAACTTTTACAAGAAAATTCTCTAGCAAAATGCCAGGCACTTACATGCTTATGGA 433
                                                                                                                                                                                                                                                                                                                                               361 TGAGAAAACTTTTACAAGAAAATTCTCTAGCAAAATGCCAGGCACTTACATGCTTATGGA 420
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                                              14 GTCGGAAAAAAAAAAAAAGCTTGTATCGTTTTCGTTGCTCTTGTCGCTCTATGCTTAAT 73
                                                                   1 Gregorarararagecrigrarestriceriscicirerescrinari 60
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                        Gaps
                       0;
  DB 21; Length 852;
                       Indels
Score 834.8; DB 2:
Pred. No. 6.4e-198
0; Mismatches 7
 96.0%;
            Best_Local Similarity 99.2
Matches 839; Conservative
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Bivalve mollusc; apopholasin; bioluminescent oxidative indicator protein; BOIP; light emission; pholasin; oxygen; chemiluminesce; cancer cell; hyperactive cell; rheumatoid arthritis; inflammatory disease; ss.
GACAACTGGTCGTTACCAGACACCCTATAACGTGTCCTCATCAATAATGTGTAAAACAGAA 793
                                    794 ATAATCGATAGAATATTGAAAATAAAATGTTAATAAACACTGGTTGAAAATATGAAAAAA 853
                                                                                                                                                                                                                                                                                                                                                                                                   encode the apophoprotein
for detecting location
in living cells and
                                                                                                                                                                                              PCR amplified genomic sequence of apopholasin DNA.
                                                                                                                                                                                                                                                                                                                                                                                                   Novel recombinant nucleic acid molecules that of pholasin or its homologous sequence useful and measurement of oxygen and its metabolites
                                                                                                                                                                                                                                                                                                                                             (UYWA-) UNIV WALES COLLEGE OF MEDICINE.
                                                                                                                                        AAA15214 standard; cDNA; 818 BP.
                                                                                                                                                                                                                                                                                                          99WO-GB03654.
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                                                                                                                                                                             (first entry)
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                                                                         854 AAAAAA 859
                                                                                           841 AAAAAA 846
                                                                                                                                                                                                                                                     Pholas dactylus.
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Disclosure; Fig 6; 49pp; English.

The present sequence represents a PCR amplified genomic sequence of apopholasin DNA. The protein is a bioluminescent oxidative indicator protein (BOIP). Changes in light emission of pholasin enable oxygan or its metabolites to be detected and quantified in live cells, organelles or on the outer or inner surface of the plasma membrane, or within an organ of a live organism without the need to break them open or the need to separate bound and free fractions. This also enables an enzyme producing oxygen or one of its metabolites to be detected and quantified. The BOIP is used for the detection, diagnosis or measurement of oxygen or its metabolites intracellularly or extracellularly. The BOIP includes a signal peptide whose target is set to a predetermined extra or intracellular site. The light emission preferably takes place in the absence of the luciferase. Pholasin is also useful as a protein or a DNA label or in genetic entertainment which involves adding pholasin to drink such as beer, cola, soft drinks and spirits to make them glow since pholasin is able to chemiluminesce at a wide range of toys and other constraining devices. BOIP nucleic acids can be used for detection and location of abnormal cells such as cancer cells, hyperactive cells in rheumatoid arthritis and other inflammatory diseases, cells infected with a pathogen, damaged cells, and measurement and location of enzymes.

Bivalve mollusc; apopholasin; bioluminescent oxidative indicator protein; BOIP; light emission; pholasin; oxygen; chemiluminesce; cancer cell; hyperactive cell; rheumatoid arthritis; inflammatory disease; ss.

Location/Qualifiers 28..705 /*tag= a /product= "apopholasin"

WO200028025-A1

Pholas dactylus

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                                                TGGCTTGTATCGTTTCGTTGCTCTTGTCGCTCTATGCTAATGCAACCGGGTTCCGGTG
                                                       AGGAAGTACAATGCGCGATGAATTGGACACAAGCTAATGAATATGTGTTCAACGTGGACT
                                                                                        GGAGTAACGACACGCAGTCATGTGTAACAAGAAAAACAATCTTCTTCGAGGTTGGTGGAG
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                                                                                                                                             TGGGGCTGTGTCGGATTGAACGGGCCGGCCCAGGTACCACAAAAGCCGTCTGGATTAACT
                                                                                                                                                                                                                                           GAAAATTCTCTCTAGCAAAATGCCAGGCACTTACATGCTTATGGACGTGCGCCTACAAGGG
                                 Gaps
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                 Length 818;
                                Indels
BP; 258 A; 156 C; 203 G; 201 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94.0%; Score 818; DB 21; 100.0%; Pred. No. 9.6e-194; ive 0; Mismatches 0;
              Query Match
Best Local Similarity 100.0
Matches 818; Conservative
Sequence 818
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is used for the detection, diagnosis or measurement of oxygen or its metabolites intracellularly or extracellularly. The BOTP includes a signal peptide whose target is set to a predetermined extra or intracellular site. The light emission preferably takes place in the absence of the ludiferase. Pholasin is also useful as a protein or a DNA label or in genetic entertainment which involves adding pholasin to drink such as beer, cola, soft drinks and spirits to make them glow since pholasin is able to chemiluminesce at a wide range of plf (3-10). It can also be added to foodstuffs and in a wide range of plg (3-10). It can be called to calls and in a wide range of toys and other entertaining devices. BOIP nucleic acids can be used for detection and location of abnormal calls such as cancer cells, hyperactive cells in rheumatoid arthritis and other inflammatory diseases, cells infected with a pathogen, damaged cells, and measurement and location of enzymes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel recombinant nucleic acid molecules that encode the apophoprotein of pholasin or its homologous sequence useful for detecting location and measurement of oxygen and its metabolites in living cells and
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0; Mismatches 3;
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                                                                                                                                                                                                                                         (UYWA-) UNIV WALES COLLEGE OF MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 3; Fig 1; 49pp; English.
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Best Local Similarity 99.4
Matches 813; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-387420/33.
P-PSDB; AAY93251.
                                                                            35-NOV-1999;
                                                                                                                                                        07-NOV-1998;
18-MAY-2000.
                                                                                                                                                                                                                                                                                                                          Campbell AK;
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CDNA sequence from clone 3 encoding apopholasin.

(first entry)

04-SEP-2000

AAA15212;

AAA15212
ID AAA1
XX
AC AAA1
XX
XX
DT 04-S
XX
XX
XX
XX

BP

AAA15212 standard; cDNA; 816

RESULT

us-09-831-142b-1.rng

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The present sequence represents a PCR amplified genomic sequence of apopholasin DNA. The protein is a bioluminescent oxidative indicator protein (BOLP). Changes in light emission of pholasin enable oxygen or trabbolites to be detected and quantified in live cells, organeles or on the outer or inner surface of the plasma membrane, or within an organ of a live organism without the need to break them open or the need to separate bound and free fractions. This also enables an enzyme producing oxygen or one of its metabolites to be detected and quantified. The BOLP is used for the detection, diagnosis or measurement of oxygen or its metabolites intracellularly or extracellularly. The BOLP includes a signal peptide whose target is set to a predetermined extra or intracellular site. The light emission preferrably takes place in the nitracellular site. The light emission preferrably takes place in the absence of the luciferase. Pholasin is also useful as a protein or a DNA label or in genetic entertainment which involves adding pholasin to drink such as beer, cola, soft drinks and spirits to make them glow since pholasin is able to chemiluminesce at a wide range of pN (3-10). It can entertaining devices. BOLP nucleic acids can be used for detection and location of abnormal cells such as cancer cells, hyperactive cells in the metalogen, damaged cells, and measurement and location of enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 TATGCTTAATGCAACCGGGTTCCGGTGAGGAAGTACAATGCGCGATGAATTGGACACAAG 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAGACGGAACTGAGAAAACTTTTACAAGAAAATTCTCTAGCAAAATGCCAGGCACTTACA 423
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                         is recombinant nucleic acid molecules that encode the apophoprotein pholasin or its homologous sequence useful for detecting location measurement of oxygen and its metabolites in living cells and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAACAATCTTCTTCGAGGTTGGTGGAGAAATTGCCCGGCTAGTTGACTACAGACCACAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 726 BP; 226 A; 145 C; 185 G; 169 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 725; DB 21;
Pred. No. 1.3e-170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                       6; 49pp; English.
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Best Local Similarity 99.9
Matches 725; Conservative
2000-387420/33
                                              pholasin or its
                                                                                                       Fig
                                                                                                       Disclosure;
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                                                                                       298
                                                                         GAAAAACCATCTTCTTCGAGGTTGGTGAGAAAATGCCCGGCTAGTGACTACAGACACC
                                                                                                                                                                                                                                                            661 ACGAGGCTGAAGACACCGTCAGAAACTGGAGAATTCTTCTGGTAGATCTATCAGACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTTTTATCAGCAGGACAACTGGTCGTTACCAGACACCTATAACGTGTCCTCAATAAT
               CAGGTACCACAAAAGCCGTCTGGATTAACTGGAGTAACGACACGCAGTCATGTGTAACAA
                                                                                                                        GAAAAACAATCTTCTTCGAGGTTGGTGGAGAAATTGCCCGGCTAGTTGACTACAGACCAC
                                                                                                                                                                                  AGGAAGACGGAACTGAGAAAACTTTTACAAGAAATTCTCTAGCAAAATGCCAGGCACTT
                                                                                                                                                                                                 ACATGCTTATGGACGTGTGCGCTACAAGGGACGCTGATGATAAATGCATCGAAGGCACAA
                                                                                                                                                                                                                                                                                                      TTGTGGTGACAGTCAGGGTGTCCCTATATGACGAAGATAACAATGGTAATGGATGAAG
                                                                                                                                                                                                                                                                                                                                                                GTAAGGTGATTCCATCTGAGACAATCGAGGATGATATCAAGGACTGTGGGGCTCTTAGACC
                                                                                                                                                                                                                                                                                                                                                                                                                          AAGATGTTGAACTCGATTATACGTGGACTCAAAACGAGTGTGTTTACCAGACACAGTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTTTTATCAGCAGGACAACTGGTCGTTACCAGACACCTATAACGTGTCCTCATCAATAAT
 GTGTAAAACAGAAATAATCGATAGAATATTGAAAATAA 818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCR amplified genomic sequence of apopholasin DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDICINE
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                                             594 TTAGACCAAGATGTTGAACTCGATTATACGTGGACTCAAAACGAGTGTGATCTACCAGAC 653
                                                                                                                                                                                                           713
                                                                                                                                                                                                                                                                                                                                                                 714 CAGACTACTTTTATCAGCAGGACAACTGGTCGTTACCAGACACCTATAACGTGTCCTCAT 773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   774 CAATAATGTGTAAAACAGAAATAATCGATAGAATATTGAAAATAAAATGTTAATAAACAC
                                                                                                                                                                                                   654 ACAGTAGACGAGGCTGAAGACACCGTCAGAAACTGGAGAATTCTTCTGGTAGATCTAT
                                                                                                                                                                                                                                                                              3998 TCCCAAACTTCCGCTAAAAAAAAAAAAATATTTACTAATTACTTCACATAAAATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; gene therapy; neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; renal disorder; proliferative disorder; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          834 TGGTTGAAATATGAAAAAAAAAAAAAAAAAACT 866
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human cDNA SEQ ID NO: 161.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200154474-A2.
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14-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L7-MAR-2000;
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14-AUG-2000;
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                                         AGGCTGAAGACACACCGTCAGAAACTGGAGAATTCTTCTGGTAGATCTATCAGACTACTT 723
                                                                                                                                                                                                                                                                                                               TTATCAGCAGGACAACTGGTCGTTACCAGACACCTATAACGTGTCCTCATCAATAATGTG 783
                                                                                                                                                                                                                                                                                                                                                     AGGCTGAAGACACCGTCAGAAACTGGAGAATTCTTCTGGTANATCTATCAGACTACTT
ATGTTGAACTCGATTATACGTGGACTCAAAACGAGTGTGATCTACCAGACACAGTAGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; immune system disease, cytosine methylation; antiasthmatic; antiatreficoscherotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmologica; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antihammatory; cancer; eye disease, arteriosclerosis; anaemia; acute myeloid leukaemia; Alraheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 9810 BP; 2961 A; 79 C; 2101 G; 4669 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immune system associated gene SEQ ID NO: 400.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
ABL3427/c
ID ABL32427 standard; DNA; 9810 BP.
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01-SEP-2000; 2000DE-1043826.
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Best Local Similarity 48.4
Matches 132; Conservative
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                                                                                                                                                     664
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02-OCT-2000; 2000US-236802P

02-OCT-2000; 2000US-23703PP

02-OCT-2000; 2000US-23703PP

02-OCT-2000; 2000US-23703PP

13-OCT-2000; 2000US-23993FP

13-OCT-2000; 2000US-24193FP

20-OCT-2000; 2000US-24178FP

20-OCT-2000; 2000US-24178FP

20-OCT-2000; 2000US-24178FP

20-OCT-2000; 2000US-24178FP

20-OCT-2000; 2000US-24178FP

20-OCT-2000; 2000US-2418FP

20-OCT-2000; 2000US-2418FP

20-OCT-2000; 2000US-2417FP

20-OCT-2000; 2000US-2417FP

20-OCT-2000; 2000US-2417FP

20-OCT-2000; 2000US-24617FP

20-OCT-2000; 2000US-24647FP

20-OCT-2000; 2000US-24647FP

20-OCT-2000; 2000US-24647FP

08-NOV-2000; 2000US-24647FP

08-NOV-2000; 2000US-246528P

08-NOV-2000; 2000US-246528P

08-NOV-2000; 2000US-246528P

08-NOV-2000; 2000US-246528P
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2000US-229287P.
2000US-229343P.
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2000US-230438P.
2000US-231242P.
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2000US-231244P.
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2000us-232397P.
2000us-232398P.
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2000US-232401P.
2000US-233063P.
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2000US-233065P.
2000US-234223P.
2000US-234274P.
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2000US-236368P.
2000US-236369P.
2000US-236370P.
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20000S-227182P.
20000S-227009P.
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2000US-232080P.
2000US-232081P.
                                                           2000US-226681P.
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2000US-229513P
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2000US-235484P
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08-NOV-2000;
08-NOV-2000;
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690 GGAGAATTCTTCTGGTAGATCTATCAGACTACTTTTATCAGCAGGACAACTGGTCGTTAC 749
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             750 CAGACACCIATAACGTGTCCTCATCAATAATGTGTAAAACAGAAATAATCGATAGAATAT 809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated nucleic acid molecule encoding an inflammation-associated polypeptide is used in preventing, treating or ameliorating a medical condition
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tive 0; Mismatches 80; Indels
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  20000S - 246610P
20000S - 246611P
20000S - 24520P
20000S - 24920P
20000S - 24920P
20000S - 249210P
20000S - 249211P
20000S - 249212P
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20000S - 249212P
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20000S-249300P.
20000S-25031DP.
20000S-251330P.
20000S-251988P.
20000S-25591P.
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20000S-249216P.
20000S-249217P.
20000S-249218P.
20000S-249244P.
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20000S-249265P
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Matches 95; Conservative
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08-NOV-2000;
08-NOV-2000;
17-NOV-2000;
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17-NOV-2000;
17-NOV-2000;
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17-NOV-2000;
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17-NOV-2000;
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01-DEC-2000;
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2000US-244617P.

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(BARA/)
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ABL33323/c
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                                                                                                      Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HTV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidabetic; antiuloer; anticonvulsant; antiingal; antianaemic; antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine;
                                                                                   Human polynucleotide SEQ ID NO 161.
                             ВÞ
                                                                                                                                                                                                                                                                                                                                                                                                                      14-AUG-2000; 2000US-225757P.
14-AUG-2000; 2000US-225757P.
22-AUG-2000; 2000US-22668P.
30-AUG-2000; 2000US-22924P.
01-SEP-2000; 2000US-229344P.
01-SEP-2000; 2000US-229344P.
01-SEP-2000; 2000US-229344P.
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21 SEP 2000; 2000US 23423P.
25 SEP 2000; 2000US 234997P.
27 SEP 2000; 2000US 234997P.
27 SEP 2000; 2000US 234997P.
29 SEP 2000; 2000US 23634P.
29 SEP 2000; 2000US 23636FP.
29 SEP 2000; 2000US 23636FP.
29 SEP 2000; 2000US 23636FP.
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28-UNA-2000) 2000US-14868P.
07-UNL-2000) 2000US-214868P.
11-UL-2000) 2000US-216880P.
11-UL-2000) 2000US-21489P.
11-UL-2000) 2000US-21489P.
14-ULL-2000) 2000US-218290P.
26-ULL-2000) 2000US-22859P.
14-AUG-2000) 2000US-22859F.
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14-AUG-2000; 2000US-22526FP.
14-AUG-2000; 2000US-225268P.
14-AUG-2000; 2000US-225270P.
14-AUG-2000; 2000US-225447P.
                          ABV83832 standard; cDNA; 758
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                                                                 09-DEC-2002 (first entry)
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                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                               11-JUL-2002
                                              ABV83832;
                                                                                                                                                                        gene; ss.
          RESULT 8
                    ABV83832
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The invention relates to novel genes (ABV83682-ABV84101) and proteins (ABB66710-ABP67129) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple solerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular discorders such as myocardial isohaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and marrow, but was obtained in electronic format directly format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 690 GGAGAATTCTTCTGGTAGATCTATCAGACTACTTTTATCAGCAGGACAACTGGTCGTTAC 749
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; immune system disease; cytosine methylation; antiasthmatic;
antiarteriosclerotic; antianaemic; cytostatic; nootropic;
neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 161; 369pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                          Barash SC;
   2000US-249299P.
2000US-251856P.
2000US-251868P.
                                                                                                   2000US-251869P
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                                                                                                                                                            ROSEN C A.
RUBEN S M.
BARASH S C.
                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-681727/73.
P-PSDB; ABP66860.
17-NOV-2000;
08-DEC-2000;
08-DEC-2000;
                                                                                                   08-DEC-2000;
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WPI; 2001-662795/76.
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                       16-MAR-2000;
                                                     18-JUL-2000;
                                           09-JUN-2000;
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ABA93725
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides a number of human immune system associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                             758 TATAACGTGTCCTCATCAATAATGTGTAAAACAGAAATAATGGATAGAATAT 817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytostatic; carcinogen; pharmacodyanamic marker; gene; ss.
                                                                                                                                                                                                                                                                                                            genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                       Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
        antiinflammatory, cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy, neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                   5.3%; Score 46.2; DB 24; Length 9741; 64.5%; Pred. No. 0.22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9741 BP; 2623 A; 195 C; 1863 G; 5060 T; 0 other;
                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 1296; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                         38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 0.22;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human prostate expression marker cDNA 59045.
                                                                                                                                                                                                 ×
                                                                                                                                                                                                Berlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABV59054 standard; cDNA; 360
                                                                                                                         02-JUL-2001; 2001WO-EP07537.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-FEB-2001; 2001WO-US05171.
                                                                                                                                              30-JUN-2000; 2000DE-1032529
01-SEP-2000; 2000DE-1043826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 64.5
Matches 69; Conservative
                                                                                                                                                                                                Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; prostate cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pharmacogenomic marker;
                                                                                                                                                                           (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                             cytosine methylation
                                                                                                                                                                                                                   WPI; 2002-130909/17.
                                                                                 WO200200928-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200160860-A2.
                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-SEP-2002
                                                                                                      03-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABV59054;
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                        gene; ds
                                                                                                                                                                                                olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient, (c) assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     682 CAGAAACIGGAGAATICITCIGGIAGAICIAICAGACIACITITATCAGCAGGACAACIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               742 GTCGTTACCAGACACCTATAACGTGTCCTCATCAATAATGTGTAAAACAGAAATAATCGA

    is also useful as a pharmacodyanamic or pharmacogenomic marker.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 45.6; DB 23; Length 360;
Pred. No. 0.11;
0; Mismatches 89; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human differentiation/development cDNA clone amy2_2b19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 360 BP; 200 A; 56 C; 45 G; 59 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 11322-11323; 11750pp; English.
                                                                                                                                                                                                                                          (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                             Schlegel R, Endege WO, Monahan JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABA93725 standard; cDNA; 3028 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.2%;
                      20000S-189862P.
20000S-207454P.
20000S-211314P.
20000S-219007P.
2000US-183319P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  862 AAACTCGA 869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     284 AAAAACAA 291
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741

Wiemann S;

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682 CAGAAACTGGAGAATTCTTCTGGTAGATCTATCAGACTACTTTTATCAGCAGGACAACTG 741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76 CAGAAACTATAACATTCAATAGTGTGTGTGTGTGTGTGCTTAGCTCACCTGGATATACC 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:

(a) assessing whether a patient is afflicted with prostate cancer;

(b) monitoring the progression of prostate cancer in a patient;

(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;

(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;

(e) selecting a composition for inhibiting prostate cancer in a patient;

(f) assessing the prostate cell carcinogenic potential of a compound;

(g) determining whether prostate cancer has metastasized in a patient;

(h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 742 GICGITACCAGACACCTATAACGIGTCCTCATCAATAATGIGTAAAACAGAAATAATCGA 801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (1) is also useful as a pharmacodyanamic or pharmacogenomic marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene therapy; cancer status prediction; cancer; ds; malignancy evaluation; drug design; antisense nucleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human cancer status prediction method-related DNA sequence #19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ## Match 5.2%; Score 45.4; DB 23; Length 488; Local Similarity 53.0%; Pred. No. 0.14; hes 97; Conservative 0; Mismatches 86; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 488 BP; 229 A; 100 C; 67 G; 92 T; 0 other;
                                                                                                                                                           (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 11298; 11750pp; English.
                                                                                                                                                                                                           Schlegel R, Endege WO, Monahan JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAL50827 standard; DNA; 2091
                   2000US-189862P.
2000US-207454P.
2000US-211314P.
                                                                                       2000US-219007P.
2000US-255281P.
2000US-183319P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                       WPI; 2001-662795/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  862 AAA 864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAA 258
                                                                                         18-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                        16-MAR-2000;
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                                                                   09-JUN-2000;
                                                25-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           802
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human;
cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2826 TCTGTTGACCTTGTTGATTGAGCATGACTACTAAATATTATGTAATAAAAAGCATTTGTC 2885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   709 TCTATCAGACTACTTTTATCAGCAGGACAACTGGTCGTTACCAGACACCTATAACGTGTC 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        769 CICAICAAIAAIGIGIAAAACAGAAAIAAICGAIAGAAIAIIGAAAAIAAAAIGIIAAIA, 828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes assemblages and computer readable media comprising novel human cDNA sequences and clones derived from human feetal brain, foetal Kidney, melanoma, testis and amygdala cDNA libraries. ABA93702 to ABA93766 represent human cDNA sequences from the present invention which encode the proteins given in ABB0562 to ABB05729. The human cDNA sequences and clones can be used in gene therapy. The clones may be used in a variety of applications, for example they may be used in profiling assays, for providing large example they may be used in profiling assays, for providing large of human genetic material for implementing large-scale screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cytostatic; carcinogen; pharmacodyanamic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                 Human cDNA sequences and clones derived from human fetal brain, fetal kidney, melanoma, testis and amygdala cDNA libraries, useful in genetic screening and therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                strategies and for treating diseases via gene therapy procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    h 5.2%; Score 45.6; DB 24; Length 3028; Sinilarity 55.8%; Pred. No. 0.21.
87; Conservative 0; Mismatches 69; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3028 BP; 1151 A; 518 C; 615 G; 744 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2946 papapapapapapapapapapapapapapapapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               829 AACACTGGTTGAAATATGAAAAAAAAAAAAAAAA 864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human prostate expression marker cDNA 58900.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 160-161; 611pp; English.
                                                                                                                                                                                                           (GEHU-) GERMAN HUMAN GENOME PROJECT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABV58909 standard; cDNA; 488
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                                                                                                                 25-APR-2001; 2001WO-IB02050.
                                                                                                                                                             25-APR-2000; 2000US-199380P
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                                                                                                                                                                                                                                                                                                  WPI; 2002-055860/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; prostate
pharmacogenomic
                                                                                                                                                                                                                                                                                                                        P-PSDB; ABB05687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200160860-A2
                     WO200198454-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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Query Match Best_Loca

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ABV58909

RESULT 12 ABV58909

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New methods for screening drug candidates are described which comparise adding a drug candidate to a cell that expresses a protein selected from ECHI, ECA2, ECJ7, ECMI, ECN5, ECO2, ECG5, ECS2, ECX2 and ECY3 or their fragments and determining the effect of the drug on the expression of those proteins. Antibodies to breast cancer genes (specifically ECHI or its fragment (ECHIP2)) are useful for inhibiting and treating breast cancer in individuals who are non-responsive to anti-oestrogen and positive for oestrogen receptor. Compositions comprising ECHI or a nucleic acid encoding The antibodies are also useful for the diagnosis and prognosis of breast cancer and for screening compositions which modulate the breast cancer phenotype. The method allows rapid and simple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Screening drug candidates for their ability to modulate breast cancer by contacting the drug to a cell expressing an expression profile gene and determining modulation of expression of the gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           682 CAGAAACTGGAGAATTCTTCTGGTAGATCTATCAGACTACTTTTATCAGCAGGACAACTG
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Pred. No. 0.23;
0; Mismatches 86; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2710 BP; 851 A; 489 C; 525 G; 845 T; 0 other;
                                                                                                                                /*tag= a
/product= BCR2 protein
                                                                   Location/Qualifiers
10..909
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (EOSB-) EOS BIOTECHNOLOGY INC
                                                                                                                                                                                                                                                                                                                                                                                                990S-0268865.
990S-0439878.
990S-0440370.
990S-0440493.
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99US-0450810.
99US-0453137.
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Best Local Similarity 53.0%;
                                                                                                                                                                                                                                                                                                                                         L5-MAR-2000; 2000WO-US06952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-MAR-2000; 2000US-0453137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mack D, Gish KC;
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                                                                                                                                                                                                                      WO200055629-A2
         Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention comprises a method for predicting cancer status. The method involves: measuring expression doses of genes obtained from specimens; selecting at least one gene as the gene for an assay; using the measurement results on expression doses of the selected genes for multivariate analysis; and classifying the specimens in analogous groups with results of the multivariate analysis on expression opatterns of the genes. The method of the invention is useful for predicting cancer, which is applicable in gene therapy for evaluating cancer malignancy with data therapy to treat cancer). The present DNA sequence represents a human nucleic acid of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1908 CAGAAACTATAACATTCAATAGTGTGTGTCAAAGTGTGCTTAGCTCACCTGGATATACC 1967
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Computer-aided statistical method for predicting cancer, applicable in gene therapy for evaluating cancer malignancy with data for use in drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              742 GTCGTTACCAGACACCTATAACGTGTCCTCATCAATAATGTGTAAAACAGAAATAATCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antibody; oestrogen receptor; anti-oestrogen; immune response; lymph node; metastases; tumour; BCR3; BCQ8; BCQ5; BCH1; BCN1; BCN2; BCN5; BCN5; BCX3; B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2091 BP; 696 A; 344 C; 392 G; 659 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 167-169; 182pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                      Matoba
                                                                                                                                                                                                                                                                                                   (DNAC-) DNA CHIP RES INC.
(HISF ) HITACHI SOFTWARE ENG CO LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                Kato K, Iwao K, Noguchi S,
                                                                                                                         07-MAR-2002; 2002WO-JP02153.
                                                                                                                                                                                14-MAR-2001; 2001JP-0073063.
06-APR-2001; 2001JP-0108503.
02-AUG-2001; 2001JP-0234807.
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WO200272828-A1
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Matches

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RESULT 14 AAA54132

Gaps

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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer, Alzheimer, Alzheimer, Alzheimer, Alzheimer, adiasease and inflammatoryulearative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps . 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 785 AAAACAGAAATAATCGATAGAATATTGAAAATAAAATGTTAATAAAACACTGGTTGAAATA 844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine methylation
                                                                                                                                                                                      Human; immune system disease; cytosine methylation; antiasthmatic; antiatreficoscleroftic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antialmamatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.2%; Score 45; DB 24; Length 17294; 70.6%; Pred. No. 0.52; ative 0; Mismatches 25; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 17294 BP; 5081 A; 203 C; 3600 G; 8410 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 960; 32pp + Sequence Listing; German.
                                                                                                                                                    Human immune system associated gene SEQ ID NO: 960.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Olek A, Piepenbrock C, Berlin K;
                                     ABL32987 standard; DNA; 17294 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-JUL-2001; 2001WO-EP07537.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
                                                                                                            26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-130909/17.
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Matches 60; Conserv
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                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                     03-JAN-2002.
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                                                                                                                                                                                                                                                                                                                            gene; ds.
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RESULT 15
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Search completed: August 22, 2003, 04:54:50 Job time : 302 secs

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Result

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Sequence 19, Appl
Sequence 8, Appli
Sequence 8, Appli
Sequence 10, Appl
Sequence 12, Appl
Patent No. 5215909
                                                                                                                                                                                                                                    Sequence 98,
Sequence 25,
Sequence 41,
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Sequence 13,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
COMPUTER: ISP PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Realease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: BORNER, F. APPLICANT: SCHEIFLINGER, F. APPLICANT: SCHEIFLINGER, F. APPLICANT: FALKNER, F. G. TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
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US-09-602-877A-95
US-09-489-847-89
US-09-372-42A-19
US-08-300-903A-8
US-08-88-197-8
US-08-545-196B-10
US-08-545-196B-12
5215909-9
US-09-202-904A-13
US-09-202-904A-13
US-09-128-155-17
US-09-128-155-17
US-09-128-155-17
US-09-123-4645-11
US-09-243-560B-1
US-09-243-560B-1
US-09-243-560B-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
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INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
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STRANDEDNESS: single
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Patent No. 5168051
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Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-955-01BC-1
US-08-697-766A-1
US-09-053-899-9
US-09-057-137-2
US-09-344-441-2
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US-09-489-847-38
US-08-553-619B-8
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US-08-280-443-1
US-08-457-459-1
US-08-555-678-1
PCT-US95-02275-1
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US-09-489-847-23
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Sequence:
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745 GITACCAGACACCIATAACGIGTCCTCATCAATAATGIGTAAAACAGAAATAATCGATAG 804
                                                                                                                                                                                                                                                                                  Sequence 1. Application US/09801052
Patent No. 636842
GENERAL INFORMATION:
APPLICANT: BERALEY, Ellen
TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
TITLE OF INVENTION: PROTEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
FILE REFERENCE: CLO01045
CURRENT APPLICATION NUMBER: US/09/801,052
CURRENT FILING DATE: 2001-03-08
NUMBER OF SEQ ID NOS: 5
                                                                                                                                                                                                           742 GTCGTTACCAGACACCTATAACGTGTCCTCATAATGTGTTAAAACAGAAATAATCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   805 AATATIGAAAATAAAAIGITAAIAAAACACIGGITGAAAHATAGAAAAAAAAAAAAAA
                                                                                                                                                                            Gaps
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                                                                                                                                    DB 4; Length 2665;
0.019;
ches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive/6300 Sears Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49;
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Fatent No. 6392471
Fatent INFORMATION:
APPLICANT: Schmandt, et al.
TITILE OF INFORTION: NOVEL SHC BINDING PROTEIN
TITILE OF INFORMES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 41.6; DB
Pred. No. 0.04;
0; Mismatches
                                                                                                                                      Score 43; DB 4
Pred. No. 0.019
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: United States of America ZIP: 60606-6402
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                                                                                                                                      4.9%;
                                                                                                                                    Query Match
Best Local Similarity 59.33
Matches 73; Conservative
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                          MOLECULE TYPE: CDNA FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                 2646 AAA 2648
                                                                                                                                                                                                                                                                                                                                                         862 AAA 864
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US-09-801-052-1
                                                             ; NAME/KEY;
; LOCATION:
US-08-971-089-5
           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1872
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US-09-363-708-3
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Matches
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TITLE OF INVENTION: NUCLEIC ACID ENCODING
TITLE OF INVENTION: SCHWANNOMIN-BINDING-PROFEINS AND PRODUCTS RELATED THERETO
                                                                                                                                                       292 GIGTAACAAGAAAAACAATCITCGAGGTIGGTGGAGAAATIGCCCGGCTAGTIGACT 351
                                                                                                                                                                                                     412 CAGGCACTTACATGCTTATGGACGTGTGCGCTACAAGGGACGCTGATGATAAATGCATCG 471
                                                                                                                                352 ACAGACCACAGGAAGACGGAACTGAGAAACTTTTACAAGAAAATTCTCTAGCAAAATGC 411
                                                                                                                                                                                                                                                                            472 AAGGCACAATTGTGGGTGACAGTCAGGGTGTCCCTATATGACGAAGATAACAATGGTGTAA 531
                                                                                                                                                                                                                                                                                                                                                   532 IGGATGAAGGTAAAGGTCATTCTGAGACAATCGAGGATGATATCAAGGACTGTGGGC 591
                                                                                                                                                                                                                                                                                                                                                                                                                          592 TCTTAGACCAAGATGTTGAACTCGATTATACGTGGACTCAAAACGAGTGTGATCTACCAG
                          Gaps
                          ó
Best Local Similarity 4.5%; Pred. No. 0.00011;
Matches 18; Conservative 220; Mismatches 164; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   652 ACACAGTAGACGAGGCTGAAGACACACGTCAGAAACTGGAG 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL & FLORES, LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-CE 2862
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PRICR APPLICATION DATA:
APPLICATION NUMBER: US 60/030,987
FILING DATE: 15-NOV-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/08971089 Patent No. 6376174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Ramos, Robert T. REGISTRATION NUMBER: 37,915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: (619)535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Pulst, Stefan M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 5:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 2665 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: United States ZIP: 92122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: San Diego
STATE: California
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US-08-971-089-5
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772 ATCAATAATGTGTAAAACAGAAATAATCGATAGAATATTGAAAATAAAATGTTAATAAAC 831
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                                                                                                                             / Match 4.8%; Score 41.4; DB 4; Length 2246; Local Similarity 61.7%; Pred: No. 0.05; les 66; Conservative 0; Mismatches 41; Indels 0.
                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08280443
Patent No. 5643778
GENERAL INFORMATION:
APPLICANT: Nishikura, Kazuko
TITLE OF INVENTION: Thereof
TITLE OF INVENTION: Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEB: Howson and Howson
STREET: Spring House Corporate Cntr, P.O. Box 457
CITY: Spring House
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIDM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PR PC POSYMS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                           MOLECULE TYPE: CDNA
DESCRIPTION: /desc = "mouse PAL CDNA"
US-09-083-587-3
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APPLICATION NUMBER:
FILLING DATE: 17-FEB-1994
ATTORNEY, AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE, DOCKET NUMBER: WST49AUSA
TELECOMMUNICATION: INFORMATION:
TELEPHONE: 215-540-9206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/280,443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.68;
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6671 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 64.5'
Matches 60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
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155..3832
      single
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CLASSIFICATION: 435
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  STRANDEDNESS:
TOPOLOGY: lir
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MOLECULE TYPE:
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US-08-280-443-1
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                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 6
US-08-280-443-1
                                                                                                                                    Query Match
                                                                                                                                                         Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 4.8%; Score 41.4; DB 4; Length 2246; Local Similarity 61.7%; Pred. No. 0.05; les 66; Conservative 0; Mismatches 41; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/09083587
Patent No. 6492138
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL SHC BINDING PROTEIN
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive/6300 Sears Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 233 South Wacker Drive/6300 Sears Tower CITY: Chicago
STATE: 11linois
COUNTRY: United States of America
2IP: 6060-6402
COMPUTENT SEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTEN: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentlin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/083,587
MEDIUM TYPE: Floppy disk
COMPUTE: IBA PC compatible
CONFURE: IBA PC compatible
SOFRANE: Patentin Pc-DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.30
CUBRENT APPLICATION DATA:
FILING DATE: US/09/363,708
FILING DATE:
                                                                                                                                                                  ATTORNEY AGENT INFORMATION:
NAME: Clough, David W.
REGISTATION UNDRER: 36,107
REFERENCE/DOCKET UNBER: 01017/34451
TELECOMMUNICATION INFORMATION:
TELEFRAX: (312) 474-6300
TELEFRAX: (312) 474-6300
TELEFRAX: (312) 474-6300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2246 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: CDNA; DESCRIPTION: /desc = "mouse PAL CDNA" US-09-363-708-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01017/34451
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ATTORNEY/AGENT INFORMATION:
NAME: CLOUGH, DAVIG W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (312) 474-6300
TELEFAX: (312) 474-6300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2246 base pairs
TYPE: nucleic acid
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                                                                                                                                                       CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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US-09-083-587-3
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GENERAL INFORMATION:
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; LOCATION:
US-08-555-678-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCT-US95-02275-1
                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.6%; Score 40.2; DB 1; Length 6671; 64.5%; Pred. No. 0.18; tive 0; Mismatches 33; Indels 0;
                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Nishikura, Kazuko
APPLICANT: Nishikura, Kazuko
TITLE OF INVENTION: RNA Editing Enzyme and Methods of Use
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cutr, P.O. Box 457
CITY: Spring House
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: PATCHIN PC-DOS/MS-DOS
SOFFWARE: PATCHIN DATA:
APPLICATION NUMBER: US/08/457,459
FILING DATE: 17-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/197,794
FILING DATE: 17-FEB-1994
PRIOR APPLICATION NUMBER: US 08/280,443
FILING DATE: 25-JUL-1994
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 31,215
REFIERRATION NUMBER: 31,215
REGISTRATION NUMBER: 31,215
REGISTRATION NUMBER: 31,215
FILING DATE: 215-540-9206
FILICATION NUMBER: 31,215
FILICOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9206
FILICATION NUMBER: 31,215
FILICATION NUMBER: 31,215
FILICATION NUMBER: 31,215
FILICATION NUMBER: 31,215
FILICOMMUNICATION INFORMATION:
FILICATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGHAL 6671 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6621 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6653
                                        832 ACTGGTTGAAATATGAAAAAAAAAAAAAAAAAAAA 864
              832 ACTGGTTGAAATATGAAAAAAAAAAAAAAAA 864
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                                                                                                                                                                      ; Sequence 1, Application US/08457459
; Patent No. 5677428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best_Local Similarity 64.5
Matches 60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
LOCATION: 155..3832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: unknown MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION:
US-08-457-459-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
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772 ATCAATAATGTGTAAAACAGAAATAATCGATAGAATATTGAAAATAAAATGTTAATAAAC 831
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GENERAL INFORMATION:
APPLICAMY: Wistar Institute of Anatomy &, Biology
TITLE OF INVENTION: RNA Editing Enzyme and Methods of Use
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 39
APPLICANT: Nishikura, Kazuko
TITLE OF INVENTION: RNA Editing Enzyme and Methods
TITLE OF INVENTION: of Use Thereof
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWSON and Howson
STREET: Spring House Corporate Chtr, P.O. Box 457
CITY: Spring House
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, P.O. Box 457
                                                                                                                                                                                                                                                                                                                   COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/555,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       832 ACTGGTTGAAATATGAAAAAAAAAAAAAAAA 864
                                                                                                                                                                                                                                                                                                                                                                                                                                       PELLING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/197,794
PRIOR APPLICATION NUMBER: US 08/280,443
FILING DATE: 25-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/457,459
FILING DATE: 01-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST49DUSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9206
TELEFAX: 215-540-5818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 215-540-5000 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: TRUGHH: 6671 base pairs
                                                                                                                                                                                                                                             ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best_Local Similarity 64.5
Matches 60; Conservative
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155..3832
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                 STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: CDNA
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775 AATAATGTGTAAAACAGAAATAATCGATAGAATATTGAAAATAAAATGTTAATAAACACT 834
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                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Reed, Michael J.
APPLICANT: Reed, Michael J.
APPLICANT: Reed, Michael J.
APPLICANT: Mohamath, Roadoh
APPLICANT: Mohamath, Roadoh
TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF
TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF
TITLE REPERENCE: 21011.475C.
CURRENT APPLICATION NUMBER: US/09/370,838
CURRENT FILING DATE: 1999-08-09
EARLIER PILING DATE: 1999-04-02
NUMBER OF SEQ ID NOS: 289
NUMBER OF SEQ ID NOS: 289
SEQ ID NO 151
LENGTH: 3275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4; Length 3275;
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APPLICANT: Rosen et al
TITLE OF INVERTION: 98 Human Secreted Proteins
FILE REFERENCE: PZ031P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 40; DB 4;
Pred. No. 0.15;
0; Mismatches
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CURRENT APPLICATION NUMBER: US/09/489,847

CURRENT FILING DATE: 2000-01-24

EARLIER APPLICATION NUMBER: PCT/US99/17130

EARLIER FILING DATE: 1999-07-29

EARLIER FILING DATE: 1998-07-30

EARLIER FILING DATE: 1998-08-05

EARLIER FILING DATE: 1998-08-05

EARLIER FILING DATE: 1998-08-05

EARLIER FILING DATE: 1998-08-12

EARLIER FILING DATE: 1998-08-12

EARLIER FILING DATE: 1998-08-05

EARLIER FILING DATE: 1998-08-06

equence 151, Application US/09370838
Patent No. 6444425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 38, Application US/09489847; Patent No. 6476195
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Best Local Similarity 63.5%;
Matches 61; Conservative (
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SEQ ID NO 38
LENGIH: 1048
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CORGANISM: Homo sapiens
US-09-489-847-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                  US-09-370-838-151
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US-09-489-847-38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.6%; Score 40; DB 6; Length 2671;
65.9%; Pred. No. 0.14;
tive 0; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No. 5168051
APPLICANT: DERYNCK, RIK M.A.; GOEDDEL, DAVID V.
TITLE OF INVENTION: NUCLEIC ACID ENCODING TGF-B ITS USES
NUMBER OF SEQUENCES: 21
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/389,929
FILING DATE: 04-AUG-1989
                                                                      ZIP: 19477
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCALL PRE-BASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                832 ACTGGTTGAAATATGAAAAAAAAAAAAAAA 864
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                                                                                                                                                                                                                                                                      CLASSITCATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/280,443
FILING DATE: 35-501-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/197,794
FILING DATE: 17-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
RESTERRUZE/DOCKET NUMBER: 31,215
REFERENCE/DOCKET NUMBER: 31,215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9206
TELEFAX: 215-540-5818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 671 Dasse pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 65.99
Matches 58; Conservative
    Spring House
Pennsylvania
Y: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
LOCATION: 155.,3832
PCT-US95-02275-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LENGTH: 2671
5168051-9
                                                                    19477
    CITY: Spr
STATE: Pe
COUNTRY:
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Matches
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Janet D. Robishaw, Charles Kunsch
VENTION: cDNA Clones Encoding Human G Protein
VENTION: Subunits
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 56.6'
Matches 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 APPLICANT: Janet D. Robi
TITLE OF INVENTION: CDMA
TITLE OF INVENTION: SCHOOL
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE:
STREET:
                                                                                                                                                                                                                                                                                                                                     Herewith
                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: Nucleic Acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 02109-1875
COMPUTER READABLE FORM:
                                                                                                                                                                                                          COMPUTER READABLE FORM:
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884 AAAAAAA 892
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         856 AAAAAAAA 864
                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
FILING DATE: Herewi
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STATE: MASSAGLAL
COUNTRY: USA
TD: 02109-1875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: Linear; ANTI-SENSE: NO PCT-US95-06406A-21
                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
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US-08-955-918C-1
                                                                                                                                                                       COUNTRY:
                                                                                                                                  CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME:
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                                                                                                                                                781 GTGTBABACAGBABATBATCGBTBGBABTBABATGARAATGTTBATBABCGCTGGTTG8 840
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                                                            739 CTGGTCGTTACCAGACACCTATAACGTGTCCTCATCAATAATGTGTAAAACAGAAATAAT 798
     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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   54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGINAL SOURCE: ORGANISM: Chimeric tomato spotted wilt virus S RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/08/553,619B
FILING DATE: December 1, 1995
                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Deflacm, Petrus T.
TITLE OF INVENTION: Virus Resistant Plants
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5919705artis Crop Protection
STREET: 975 California Avenue
CITT: Palo Alto
   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       137-1082/PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  841 AATATGAAAAAAAAAAAAAAACT 866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     977 AAAATGAAATAAAAACAACAAAAAT 952
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94304
COMPUTER READABLE FORM:
MEDIOM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                              RESULT 13
US-08-553-619B-8/C
; Sequence 8, Application US/08553619B
; Patent No. 5919705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 137-
TELEPHONE: 415/854-3588
TELEPAX: 415/857-1125
INPORMATION FOR SEQ ID NO: 8;
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: MAICUS-Wyner, Lynn
REGISTRATION NUMBER: 34,869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGIH: 2621 base pairs
TYPE: nucleic acid
 Conservative
                                                                                                                                                                                                                        1010 AAAAAA 1015
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PCT-US95-06406A-21
72;
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 Matches
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736 CAACIGGICGITACCAGACACCIAIAACGIGICCICCAICAAIAAIGGIGIAAAACAGAAAI 795
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Kleyn, Patrick, and Moore, Karen
ITILE OF INVENTION: RP Compositions and Therapeutic and
ITILE OF INVENTION: Diagnostic Uses Therefor
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE IABLIVE & COCKFIELD, LLP
STREET: 28 State Street
     DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb
COMPUTER: IBM 486
OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                               PCT/US95/06406A
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MEDIUM TYPE: Floppy disk

COMMPUTER: IBM PC compatible

COMMPUTER: IBM PC compatible

COMMPUTER: System PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/08/955,918C

FILING DATE: PS-NUG-1996

ATTING DATE: PS-NUG-1996

ATTING DATE: PS-NUG-1996

ATTING DATE: NUMBER: MAI ON TOTAL PROGRATION:

NAME: Mandragourse, Amy E.

REGISTRATION NUMBER: 36,207

REPREDOMNITATION HYDRAMATION:

TELECOMMUTATION 

TELECOMMUTATION HYDRAMATION:

TELECOMMUTATION HYDRAMATION:

TELECOMMUTATION HYDRAMATION:

TELECOMMUTATION:

TELECOMMUTATIO
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Search completed: August 22, 2003, 06:32:51 Job time: 75 secs

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August 22, 2003, 04:53:13 ; Search time 649 Seconds (without alignments) 3013.717 Million cell updates/sec
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2: (cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
4: (cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
4: (cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
5: (cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*
6: (cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*
7: (cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
7: (cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
8: (cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
9: (cgn2_6/ptodata/1/pubpna/USO9A_PUBCOMB.seq:*
10: (cgn2_6/ptodata/1/pubpna/USO9A_PUBCOMB.seq:*
11: (cgn2_6/ptodata/1/pubpna/USO9A_PUBCOMB.seq:*
12: (cgn2_6/ptodata/1/pubpna/USO9A_PUBCOMB.seq:*
13: (cgn2_6/ptodata/1/pubpna/USO9A_PUBCOMB.seq:*
14: (cgn2_6/ptodata/1/pubpna/USO0A_PUBCOMB.seq:*
15: (cgn2_6/ptodata/1/pubpna/USO0A_PUBCOMB.seq:*
16: (cgn2_6/ptodata/1/pubpna/USO0A_PUBCOMB.seq:*
17: (cgn2_6/ptodata/1/pubpna/USO0A_PUBCOMB.seq:*
16: (cgn2_6/ptodata/1/pubpna/USO0A_PUBCOMB.seq:*
17: (cgn2_6/ptodata/1/pubpna/USO0A_PUBCOMB.seq:*
17: (cgn2_6/ptodata/1/pubpna/USO0A_PUBCOMB.seq:*
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1517243 segs, 1124081882 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                    OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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870
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Perfect score:
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                                                                                                                                                                                                     Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

DB ID Description		14 US-10-198-846-12795 Sequence 12795											9 US-09-925-299-235 Sequence 235, App		10 US-09-761-640-2 Sequence 2, Ap	
% Query Match Length DB ID	9810	3999	758	9741	17294	802	802	6211	6040	363	11745	413	1321	1321	2852	
Query Match	5.4	5.4	5.4	5.3	5.2	ъ.	5.1	5.1	5.1	5.0	5.0	5.0	5.0	5.0	5.0	
Score	47.4	47.2	47	46.2	45	44.8	44.8	44.8	44	43.8	43.4	43.2	43.2	43.2	43.2	
Result No.	H	7	m	4	ιŲ	9	7	æ	σ	10	11	12	13	14	15	•
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Sednence sed	the Immune sapiens)	Length 9810; Indels 0; Gaps AACGAGTGTGATCTACCAGA CAACTAAAACACCATCCTAA GAATTCTTCTGGTAGATCTA AATTACTTCACATAAAATT
	with	2; Length 1; Indels AAAACGAGTG AACAACTAAA GAGAATTCTTTTTTTTTTTTTTTTTTTT
7 - 8 - 9 - 9 - 9 - 9 - 9 - 9 - 9 - 9 - 9	S Assoc	.4; DB 1 tches 14 CGTGGACTC CGTGAACTC CAGAAACTG
US-10-13 US-10-144 U	ALIGNM ian ian ian 10/311,46 6 P01/0753 032529.7	Score 47 Pred. No 0; Mismal TCGATTATA TAABATATATA ACACACCGTC ACACACCGTC ACACACAAA
	18/100 106A1 1hris: 1hris: 108 10 108 108 10 108 108 10 108 108 10 108 108 108 10 108 108 108 108 108 108 108 108 108 108	4%; 4%; GAAC GAAC GAAG
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a a a a a a a a a a a a a a a a a a a	455-400/c 400, Application No. US200. INT OLEK, Ale: NT: OLEK, Ale: NT: DEPENBRUT: PERENBRIN, 18 FILING PATE: PELICATION NU TILING DATE: PELICATION NU TILING DATE: PELICATION NU TILING DATE: PELICATION NU TILING DATE: 20 PELICATION NU TILING DATE: 21 PELICATION NU TILING DATE: 22 PELICATION NU TILING DATE: 23 PELICATION NU TILING DATE: 24 PELICATION NU TILING DATE: 25 PELICATION NU TILING DATE: 26 PELICATION NU TILING DATE: 27 PELICATION NU TILING DATE: 28 PELICATION NU TILING DATE	Similarity (2) Conserv TTAGACCAA(TTTAACCTAA(TTTAACCTAA(ACAGTAGACC
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JS-09-764-853-161
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Best Local S
Matches 95
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                                              777 TAATGTGTAAAACAGAAATAATCGATAGAATATTGAAAATAAAATGTTAATAAAACACTGG 836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 ACTATGTTAATGAGTATGTAAAACATTCTTTTGCATTGATGAATTTTGTATCTGCTTCCA 124
                      714 CAGACTACTTTTATCAGCAGGACAACTGGTCGTTACCAGACACCTATAACGTGTCCTCAT 773
                                                                                               774 CAATAATGTGTAAAACAGAAATAATCGATAGAATATTGAAAATAAAATGTTAATAAACAC 833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64
                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: MILLS. CAMES
APPLICANT: WI, YORGYAO
APPLICANT: Wang, YOUZHAN
APPLICANT: WANG, YOUZHAN
APPLICANT: WANG, YOUZHAN
APPLICANT: WANG, YOUZHAN
TAPLICANT: STATIMEND. RATHINGN. RESESSMENT, PREVENTION, AND
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF BREAST CANCER
TITLE OF INVENTION: THERAPY OF BREAST CANCER
TITLE OF INVENTION: THERAPY OF BREAST CANCER
CURRENT APPLICATION NUMBER: US/10/18
CURRENT FILING DATE: 2001-07-18
NUMBER OF EQ. ID NOS: 14084
SOTWARR: FASTSEQ for Windows Version 4.0
SEQ ID NO 12795
LENGTH: 3999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               717 ACTACTTTTATCAGCAGACAACTGGTCGTTACCAGACACCTATAACGTGTCCTCATCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 0.079;
0; Mismatches 63; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPREBROE: P4206
CURRENT PLING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 939
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 161
LENGIH: 758
                                                                                                                                                                                                             3818 ITTITICATIACAAATTAAATAAAAAACCT 3786
                                                                                                                                                                        834 TGGTTGAAATATGAAAAAAAAAAAAACT 866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 837 TTGAAATATGAAAAAAAAAAAAA 864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 12795, Application US/10198846 Publication No. US20030099974A1
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Patent No. US20020090672A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 5.4%;
Best Local Similarity 57.4%;
Matches 85; Conservative C
                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION: APPLICANT: Lillie, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens
US-10-198-846-12795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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APPLICANT: OLEK, Alexander
APPLICANT: OLEK, Alexander
APPLICANT: PIEBENBROK, Christian
APPLICANT: PIEBENBROK, Christian
TITLE OF INVENTION: Use of Diseases Associated with the Immune System by Def
TITLE OF INVENTION: Cytosine methylation
TITLE OF INVENTION: Cytosine methylation
TITLE OF INVENTION: Cytosine methylation
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR FILING DATE: 2001-07-02
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: OLEX, Alexander
APPLICANT: OLEX, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Det
TITLE OF INVENTION: Cytosine methylation
FILE REPRENEUS: 5013.1014
CURRENT APPLICATION NUMBER: 105/10/311,455
CURRENT PILING DATE: 2002-12-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          758 TATAACGIGTCCICATCAATAATGIGTAAAACAGAAATAATCGATAGAATATIGAAAATA 817
                                                                                                   690 GGAGAATICTICTGGTAGAICTATCAGACTACTTTTATCAGCAGGACAACTGGTCGTTAC 749
                                                                                                                                                                                                    750 CAGACACCIATAACGIGTCCICATCAATAATGIGTAAAACAGAAATAATCGATAGAATAI 809
                                                       Gaps
                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-311-455-1296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 9741;
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Pred. No. 0.039;
0; Mismatches 80; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 46.2; DB 12;
Pred. No. 0.23;
0; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1296, Application US/10311455 Publication No. US20030143606A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 960, Application US/10311455
Publication No. US20030143606A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.3%;
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69; Conservative
                            1 Similarity 54.3 95; Conservative
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SEQ ID NO 1296
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Sequence 779, Application US/10311455
Publication No. US20030143606A1
General Information No. US20030143606A1
General Information No. US20030143606A1
General Information:
APPLICANT: DIEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
ITILE OF INVENTION: Cytosine methylation
ITILE OF INVENTION: Cytosine methylation
FILE REPERBROCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR FILING DATE: 2000-06-30
PRIOR PLILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEMON NUMBER: DE 10043826.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               769 CTCATCAATAATGTGTAAAACAGAAATAATCGATAGAATATTGAAAATAAAATGTTAATA 828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Single Nucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 805;
                                                                                                      APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Sing-
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 44.8; DB 13;
Pred. No. 0.15;
0; Mismatches 32;
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                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-02-24
PRIOR PILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/16,358
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 325720
SORTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 29968
LENGTH: 805
                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
                                                        Sequence 29968, Application US/10027632 GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 6
PRIOR FILING DATE: 1999-08-09
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Best Local Similarity
Matches 64; Conserve
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US-10-311-455-779/c
                                   JS-10-027-632-29968
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GENERAL INFORMATION:
APPLICANT: Wangy, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Delymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR PRILING DATE: 2000-01-22
PRIOR FILING DATE: 2000-04-20
PRIOR PELICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR PELING DATE: 2000-02-24
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-80
NUMBER OF SEQ ID NOS: 325720
SOUTHWARE: US 60/146,002
NUMBER OF SEQ ID NOS: 325720
                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-311-455-960
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                                                                                                                                                                                                                                                                                                                                                                   Score 45; DB 12; Length 17294;
Pred. No. 0.62;
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66.7%; Pred. No. 0.15;
tive 0; Mismatches 32;
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                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR PLING DATE: 2000-06-30
PRIOR PLING DATE: 2000-06-30
PRIOR PLING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10033 TCAACAAAAAAAAAAATAACGCTA 10009
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Best Local Similarity 66./*,
"..hes 64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        60; Conservative
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Best Local Similarity
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US-10-027-632-29967
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GENERAL INFORMATION:
APPLICANT: OLER, Alexander
APPLICANT: OLER, Alexander
APPLICANT: DESTAURCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA
TITLE OF INVENTION: Transcription
TITLE OF INVENTION: With DNA TRANSCRIPTION
CURRENT APPLICATION NUMBER: US/10/240,453
CURRENT APPLICATION NUMBER: US/10/240,453
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                                                                                                                                                                                                                                                                                                                                                722 ITTIBICAGCAGGACAACTGGTCGTTACCAGACACCTATAACGTGTCCTCATCAATAATG 781
                                                                                                                                                                                                                                                                                                                                                                                                           171 TITICICCCCTAAAATICAGCTGCTTTCAAAGCACCAGCCACTTTTACTTTTTAACAATA 112
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                                                                                                                                                                                                            Score 43.8; DB 10; Length 363;
Pred. No. 0.18;
0; Mismatches 62; Indels 0:
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                                                           TYPE: DNA ORGANISM: Bos taurus OTHER INFORMATION: CLONE ID: 50-LIB3058-012-01-K1-E10
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Pred. No. 1.3;
0; Mismatches 76;
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CURRENT PILING DATE: 2002-10-02
PRIOR APPLICATION WINBER: PCT-PE01/03973
PRIOR PILING DATE: 2001-04-06
PRIOR FILING DATE: 2001-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 350
SEQ ID NO 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                842 ATATGAAAAAAAAAAAAAAA 864
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Publication No. US20030148326A1
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Best Local Similarity 56.6%;
Matches 81; Conservative (
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Best Local Similarity
Matches 89; Conserv
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TOCATION: (9105)
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US-10-240-453-206/c
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   SEQ ID NO 11687
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Sequence 40, Application US/10311455

Publication Word Control Con
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APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagam, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
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   Length 6211;
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Pred. No. 0.66;
0; Mismatches 45; Indels
                                                                 57; Indels
Score 44.8; DB 12;
Pred. No. 0.42;
                                                                 0; Mismatches
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   5.1%;
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                                Best_Local Similarity 58.1 Matches 79; Conservative
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Best Local Similarity
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LENGTH: 6040
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   Query Match
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US-09-761-640-2
                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  794 ATAATCGATAGAATATTGAAAATAAATGTTAATAACACTGGTTGAAATATGAAAAAA 853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 43.2; DB 11; Length 413;
Pred. No. 0.28;
0; Mismatches 55; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 235, Application US/09925299
Fatent No. US2002055527A1
GENERAL INFORMATION:
FAPPLICANT: Rosen et al.
FITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FITLE REPERENCE: PALO2
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
FRICH APPLICATION NUMBER: CT_VUSO0_05883
FRICH APPLICATION NUMBER: 60/124,270
FRICH APPLICATION NUMBER: 60/124,270
FRICH APPLICATION NUMBER: 60/124,270
FRICH APPLICATION NUMBER: 1999-03-12
                                                6429 АААТСААААТААААСТТТАТАТАТАТСАААААТАААААА 6385
                                                                                                                                                                                                                           APPLICANT: HYSER, INC.

TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: REAM VARIOUS CDNA LIBRARIES
FILT REPERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT APPLICATION NUMBER: US/09/235,076
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR PILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FestSEQ for Windows Version 3.0
SEQ ID NO 7068
NAME/KET: misc_feature
LOCATION: (1313)
OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc_feature
LOCATION: (1320)
                                                                                                                                                                 Sequence 7068, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: (1)...(413)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-7068
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Best Local Similarity 57.7%;
Matches 75; Conservative (
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SEQ ID NO 235
LENGTH: 1321
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LOCATION: (1)...(413)
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                                                                                                                                         03-09-918-995-7068
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US-09-925-299-235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
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APPLICANT: WEI, Ming-Hui et al TITLE OF INVENTION: ISOLATED HUMAN PHOSPHATASE PROTEINS, TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHATASE PROTEINS, FILLE OF INVENTION: AND USES THEREOF FILE REFERENCE: CLOOO964-CIP CURRENT APPLICATION NUMBER: US/09/761,640 CURRENT FILING DATE: 2001-01-18
                                                                                                                                                                                                 761 AACGIGTCCTCATCAATAATGTGTAAAACAGAAATAATCGATAGAATATTGAAAATAAAA
                                                                                                                                                          761 AACGIGICCICAICAAIAAIGIGIAAAACAGAAAIAAICGAIAGAAIAITGAAAAIAAAA
                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1321;
                                                                  Length 1321;
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TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REPERENCE: PALIO.
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
FRIOR APPLICATION NUMBER: PCT/US00/05883
FRIOR APPLICATION NUMBER: 60/124,270
FRIOR PILING DATE: 1999-03-08
FRIOR RILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: PATCHIN VET. 2.0
SEQ ID NO 235
LENGTH: 1321
                                                                                                                                                                                                                                        Indels
                                                                                                                38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 11;
                                                                Score 43.2; DB 9;
Pred. No. 0.5;
0; Mismatches 38;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
; OTHER INFORMATION: n equals a,t,g, or c US-09-925-299-235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: (1320)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-299-235
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OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 235, Application US/09925299
Publication No. US20030040617A9
GENERAL INFORMATION:
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                                                                  5.0%;
                                                                                       Best_Local Similarity 63.5
Matches 66; Conservative
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Best Local Similarity 63.55
Matches 66; Conservative
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0; Gaps
                                                                        Query Match 5.0%; Score 43.2; DB 10; Length 2852; Best Local Similarity 58.6%; Pred. No. 0.73; Matches 75; Conservative 0; Mismatches 53; Indels 0;
; LENGTH: 2852
; TYPE: DNA
; ORGANISM: Human
US-09-761-640-2
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Search completed: August 22, 2003, 06:43:51 Job time : 652 secs

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49.4 5.7 310 9 AA230648 49.4 5.7 811 12 BI825633 48.2 5.5 385 10 BE048135 48 5.5 792 28 AZ195391 47.6 5.5 338 14 CA338213	47.6 5.5 346 12 BI500307 47.6 5.5 815 13 BU566867 47.4 5.4 349 13 BU56867 47.4 5.4 430 13 BU564850 47.4 5.4 438 14 CA337338	15 47.4 5.4 1065 29 CNSG1642T AL462183 Clone BAO 16 47.4 5.4 1121 29 CNSG1623 AL106197 Drosophil 17 47 5.4 408 4 CA779772 CA779772 RDASS1089 18 47 5.4 1102 13 BA381089 BASS1089 BASS1089 BASS1089 BASS1089 CA78975 19 46.8 5.4 289 12 BAB4688 BAB18A07 CA78978 20 46.8 5.4 978 9 AL544049 AL5	46.8 5.4 1041 14 CD051043 46.6 5.4 211 13 BQ667088 46.6 5.4 325 14 C93882	24 46.6 5.4 955 13 BU929015 25 46.6 5.4 1108 29 CNSOOTIO	27 46.4 5.3 115 9 AI399560 28 46.4 5.3 115 9 AI399560 28 46.4 5.3 1115 13 BU531671	46.2 5.3 47.7 12 BM30553 46.2 5.3 47.7 12 BM30553 46.2 5.3 935 13 BX328353 46.2 5.3 956 29 CNS014V0	46.5.3 29.5 CNSOSDCO 46 5.3 236 13 E08937940 46 5.3 375 14 CA3345987 46 5.3 553 9 ALG33429 46 5.3 669 11 AYG6474	46 5.3 808 14 CB318829 46 5.3 1264 13 BQ940146 45.8 5.3 139 12 BI814718	1 45.8 5.3 213 9 AW423994 2 45.8 5.3 225 13 BU642591	45.8 5.3 45.8 5.3	ALIGNMENTS	PRSTIT 0	03/c AL544003 FION AL544003 Homo sapie	z	KEYWORDS EST. SOURCE Homo sapiens (human) ORGANISM Homo sapiens		AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D. TITLE Full-length cDNA libraries and normalization JOURNAL Unpublished OMMENT On Feb 15, 2001 this sequence version replaced gi:12876482.		Email: segref@genoscope.ons.fr, Web : www.genoscope.ons.fr Library was constructed by Life Technologies, a division of	intrication about this cluster, see http://www.genoscope.cns.fr/ cgi-bin/cluster.cgi7seq-cSODIO04AA01QPl&cluster-8347.r. Contact : Feng Liang Email : fliang@ilfetech.com URL :
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gen Ltd.	Search time 2303 Seconds (without alignments) 9181.456 Million cell updates/sec	aaaaaaaaaaaaactcgag 870	Ď.	45562784													i by chance to have a the result being printed, e distribution.		Description	AL544003 AL544003 BI524329 603052182 C89835 C89835 Dict CB708528 AMGNNUC:S
GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen 1	 nucleic search, using sw model August 22, 2003, 01:42:03; search (without 9181.456 	US-09-831-142B-1 870 1 gaattcggcacgagtcggaaIDENTITY_NUC	Gapop 10.0 , Gapext 1.0 22781392 seqs, 12152238056 residues	r of hits satisfying chosen parameters:	seq length: 0 seq length: 2000000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	BST:* 1: em_estba:* 2: em_esthum:* 3: em_estium:*						18: em_gss_inv:* 19: em_gss_pin:* 20: em_gss_vrt:*				o. is t reater derived	SUMMARIES	Query Score Match Length DB ID	50.8 5.8 918 9 AL544003 50.2 5.8 683 12 BI524329 49.8 5.7 206 14 C89835 49.8 5.7 317 14 CB708528
	OM nucleic Run on:	Title: Perfect score: Sequence: Scoring table:	Searched:	Total number	Minimum DB Maximum DB	Post-proces	Database :					,					Pred. N score g and is		Result No. So	00 H 02 W 44

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                                                                                                                                                                                                                                                                                                                                                                                                                       681 TCAGAAACTGGAGAATTCTTGGTAGATCTATCAGACTACTTTTATCAGCAGGACAACT 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="PLACENTA COT 25-NORMALIZED"
//clone_lib="moon sapiens PlACENTA COT 25-NORMALIZED"
//orde="las strand cDNA was primed with a NoLT-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and ECOR V
sites of the pCMVSPORT 6 vector. Library was normalized."
108 c 123 g 264 t 113 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                             785 TAAAACACMAWWITITITITCCACTMWATATAIMMSNYCTIYIWTITITMMAACTATATWV 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    741 GGTCGTTACCAGACACCTATAACGTGTCCTCATCAATAATGTGTAAAAACAGAAATAATCG 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
http://image.lnl.gov
Plate: LiAM11505 row: d column: 22
                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (WGC)
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI004AA01QP1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-rémail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA. Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                            Length 918;
                                                                                                                                                                                                                                                                                                                                      Score 50.8; DB 9; Length 91
Pred. No. 3e+02;
7: Mismatches 76; Indels
                                                                                                                                                                                                                                                                                                                                      5.8%; Score 50.3; 24.4.0%; Pred. No. 3e+07; tive 27; Mismatches
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/mol_type="mRNR"
/db_xref="taxon:9606"
/clone="lake:5201637"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
Contact: Robert Strausberg, Ph.D.
                                                                               /organism="Homo sapiens"
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                                                                                                 /mol_type="mRNa"
/db_xref="taxon:9606"
/clone="CSODI004xA01"
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Homo sapiens
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                                         FEATURES
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/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6; Site_1: NotI: Site_2: BcoRV (destroyed); RNA source anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 Kb, insert size range 1-3 kb, Library is normalized and enriched for full-length clones and was. constructed by C. Gruber (Invitroyell). Research Genetics tracking code 026. Note: this is a NHAC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST 20-APR-1998
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1 (bases 1 to 206)

Morio, T., Grushihara, H., Saito, T., Ugawa, Y., Mizuno, H., Yoshida, M., Yoshino, R., Mitra, B.N., Pi, M., Sato, T., Takemoto, K.; Yasukawa, H., Williams, J., Maeda, M., Takeuchi, I., Ochiai, H. and Tanaka, Y.
Developmental cDNA in Dictyostellum discoideum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ő
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/dev_stage="blug"
/clone_lib="Dictyostellum discoideum SS (H. Urushihara)"
11 c 12 g 48 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C89835 Dictyostelium discoideum SS (H.Urushihara) Dictyostelium discoideum CSSSC15, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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Tel: 81-298-53-4664
Fax: 81-298-53-6614
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                                                                                                                                                                                                                                                                                                                                                   5.8%; Score 50.2; DB 12;
59.4%; Pred. No. 4.2e+02;
tive 0; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: hideko@biol.tsukuba.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
Context: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:44689"
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1. .206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/strain="AX4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dictyostelium discoideum
Dictyostelium discoideum
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C89835.1 GI:3059455
                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 59.4
Matches 85; Conservative
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Best Local Similarity 59.66
Matches 84; Conservative
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linear EST 04-0CT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3'], on total mouse RNA [provided by Minoru Ko, Wayne State Univ.]; double-tranded corNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. " 33 c 36 g 62 t
                                                                                                                                         Dietrich, N., Dubuque, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           694 AATTCTTCTGGTAGATCTATCAGACTACTTTTATCAGCAGGACAACTGGTCGTTACCAGA 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 AAGTATTTTTGAATACCATTAAAACTGCTTTTTTCCAGTAAATATCTGACCAACTTGTTA 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          754 CACCTATAACGTGTCCTCATCAATAATGTGTAAAACAGAAATAATCGATAGAATATTGAA 813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammala; Britheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 310)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.
                                                                                                                                                                                                                                                                                                                                                                                             Email: mouseestewatson.wustl.edu
This clone is available royalty-free through LLML; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                          Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 310;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="12.5dpc total fetus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.7%; Score 49.4; DB 9;
55.6%; Pred. No. 8.2e+02;
tive 0; Mismatches 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vector to vector length is 733
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 282.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .310
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/65"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                 Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                         The WashU-HHMI Mouse EST Project
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                                       Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Putative full length read
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="unknown"
GI:1852963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 55.6
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                            Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                        Waterston, R.
                                                                                                                                                                                                                                                              Unpublished
AA230648.1
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ORGANISM
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BI825633
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AMGNNUC:SRCS1-00022-G3-A srcs1 (10883) Rattus norvegicus cDNA clone srcs1-00022-g3 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA230648 310 bp mRNA linear EST 26-FEB-1997 mw06d10.rl Soares mouse 3NME12 5 Mus musculus cDNA clone IMAGE:669907 5' similar to gb:X51438 Mouse mRNA for vimentin (MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         676 CACCGTCAGAAACTGGAGAATTCTTCTGGTAGATCTATCAGACTACTTTTATCAGCAGGA 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         784 TAAAACAGAAATAATCGATAGAATATTGAAAATAAAATGTTAATAAAACACTGGTTGAAAT 843
                                     Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Rattus norvegicus"
//mol_type="mrRN"
//db_xref="laxon:1016"
/clone="srcs1-00022-g3"
//tissue_type="Cornea"
/clone_lib="srcs1 (1083)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Site_2: EcoRI;
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One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
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54.0%; Pred. No. 7.1e+02;
Live 0; Mismatches 87;
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Plate: 00022 row: g column: 3.
    Location/Qualifiers
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Rattus norvegicus
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                                                                                               844 ATGAAAAAAAAAAAAAAA
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Amgen EST Program.
Amgen Rat EST Program
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27 c
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CB708528
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Mammalia; Butheria; Primates; Catarrhin; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Organ brain; Vector: pcxv-SpoRT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dr primed and directionally cloned (EcoRv site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BE048135
385 bp mRNA linear EST 20-OCT-2000
tz46c11.y1 NÇI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2291636 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             778 AATGTGTAAAACAGAAATAATCGATAGAATATTGAAAATAAAATGTTAATAAACACTGGT 837
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MIH-MGC http://mgc.nci.nih.gov/.
Nätional Institutes of Health, Mammalian Gene Collection (MGC)
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
603072606F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5164560 5',
                                                                                                                                                                                                         Unpublished
Contact: Robert Strausberg, Ph.D.
Bamil: capabsrremail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MgC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                276.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="IMAGE:5164560"
/tissue_type="medulla"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 2
Location/Qualifiers
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                                                                                          Homo sapiens (human)
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                  mRNA sequence.
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KEYWORDS
SOURCE
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/mol_wrpe="mrm".complete:
/mol_wrpe="mrm".complete:
/mol_wrpe="taxon:9606"
/db_xref="taxon:9606"
/lab_lost="taxon:9606"
/lab_lost="billos"
/clone_lib="NcI_CGAP_Brn52"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Sall;
/note="Organ: prain; Vector: pCMV-SPORT6; Site_1: Sall;
/note="Organ: prain; Vector: pCMV-SPORT6; Site_1: Sall;
/note="Organ: prain; Vector: pCMV-SPORT6; Site_1: Sall;
/note="Organ: pcan; Vector: pCMV-SPORT6; Site_1: pcan; Vector: pCMV-SPORT6; pcan; Vector: pCMV-SPORT6; pcan; Vector: pCMV-SPORT6; pcan; Vector: pc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R. Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Sequencing by: Mashington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
infoctinage.lihi.gov

Insert Length: 437 Std Error: 0.00

Seq primer: -40RP from Gibco

High quality sequence stop: 369.
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SP_101 E2_605_T7A Strongylocentrous purpuratus, purple sea urchin sperm genomic BAC library Strongylocentrous purpuratus genomic clone plate=1031 Col=10 Row=N, genomic survey sequence.
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
1 (bases 1 to 385)

MCININDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCININDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NAtional Cancer Institute / National Institute of Neurological

Disorders and Stroke, Brain Tumor Genome Anatomy Project

(CGAP/BTGAP), Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherczoa; Echinozoa;
Echinoidea; Eucchinoidea; Echinacea; Echinoida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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Pred. No. 1.1e+03;
0; Mismatches 103;
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/organism="Homo sapiens"
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McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J., Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Tsagareishvilli,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Steptoe,M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BIS00307 346 bp mRNA linear EST 28-AUG-2001 rs/8d05.yl Prist pacificus mixed stage pAMP1 vl Chiapelli McCarter Pristionchus pacificus cDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: pAMP1, cDNA primed using oligo-dr primer, directionally cloned into UDG sites of pAMP1. Size selected for insert sizes ranging from 0.2-1.2 kb. Normalized to Cotl0. Primary library, non-amplified. Library constructed by M. Lovett. For more information on this library, please contact R. Tidwell (Washington University) or visit the COGENE website at http://mg.watl.edu/COGENE/."

1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         682 CAGAAACTGGAGAATTCTTCTGGTAGATCTATCAGACTACTTTTATCAGCAGGACAACTG 741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequencing Center (NISC) Clone distribution information can Clone distribution: NCI-CGAP clone distribution:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 742 GTCGTTACCAGACACCTATAACGTGTCCTCATCAATAATGTGTAAAACAGAAATAATCGA
                                            CDNA Library Preparation: CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL DNA Sequencing by: National Institutes of Health Intramural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
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                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="1st pharyngeal arch (pooled)"
/dev_stage="embryo, 4 weeks postconception"
/lab_host="DH10B"
                                                                                                                                                       found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                            info@image.Ilnl.gov
Plate: LLAM12415 row: L column:
Seg primer: M13RP1 reverse primer
Location/Qualifiers
                                                                                                                                                                                                                                                                         1. .338
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="COGENE 4PA1"
    Ph.D.
                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5610001"
                           Email: cgapbs-r@mail.nih.gov
    Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BI500307.1 GI:15339651
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CA338213 338 bp mRNA linear EST 04-NOV-2002
NISC_Lw12f01.y1 COGENE 4PA1 Homo sapiens cDNA clone IMAGE:5610001
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Cameron,R.A., Mahairas,G., Rast,J.P., Martinez,P., Biondi,T.R.,
Swatzell,S., Wallace,J.C., Poustka,A.J., Livingston,B.T., Wray
G.A., Ettensohn,C.A., Lehrach,H., Britten,R.J, Davidson,E.H. and
Hood,L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 338)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       643 ATCTACCAGACACAGTAGACGAGGCTGAAGACACCGTCAGAAACTGGAGAATTCTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                  A sea urchin genome project: Sequence scan, virtual map, and additional resources
Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)
20402566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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Pred. No. 8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 792.

Location/Qualifiers
1. 792
/organism="Strongylocentrotus purpuratus"
/mol_type="genomic DNA"
/db_xref="taxon:7668"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches 111; Indels
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Strongylocentrotidae; Strongylocentrotus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    406 t
                                                                                                                                                                                                                                           Contact: Cameron, RA, Davidson, EH, 1
Division of Biology 156-29
California Institute of Technology
Asadena California 91125, USA
Tel: (626) 395-8421
Fax: (626) 793-3047
                                                                                                                                                                                                                                                                                                                                                                                     Seg primer: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  158 g
                                                                                                                                                                                                                                                                                                                                                                              Email: acameron@caltech.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.5%; Scor.
50.0%; Pred
0;
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CA338213.1 GI:24556311
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TITLE
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McCarter"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Incte="Vector: pAMP1 (Gibco); Site_1: NotI; Site_2: SalI;
The library was constructed by Brandi Chiapelli and Dr.
James McCarter at Washington University, St. Louis. The
CARA was made by using pynabead oligo-df priming (Dynal).
PCR based library using a modified protocol from the
SMART PCR CONA Synthesis Kit from Clontech. Directionally
cloned into the UDG sites of pAMP1. "

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 815)
                                                                                                                                                                                         This clone is available royalty-free through LLML; contact the IMAGE Consortium (info@image.llnl.gov) for further information. High quality sequence stop: 339.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDNA Library Preparation: Michael Brownstein Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Linn at: http://image.llnl.gov
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National Institutes of Health, Mammalian Gene Collection (MGC)
Ontpublished
Contact: Robert Strausberg, Ph.D.
Email: ogapbs.r@mail.nih.gov
Tissue Procurement: NCI
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           Unpublished
Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Fax: 314 286 1810
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AGENCOURT_10397234 NIH_MGC_141 Homo sapiens cDNA clone
IMAGE:6606315 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 47.6; DB 12; Length 346;
Pred. No. 1.4e+03;
0; Mismatches 49; Indels 0
Washington Univ. Nematode EST Project, 1999
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/mol_type="mRNA"
/dol_tref="taxon:54126"
/dev_staqe="mixed"
/lab_host="DH10B"
                                                                                                                                                                         Email: est@watson.wustl.edu
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/clone="IMAGE:606315"
/tissue_type="mixed (pool of 40 RNAs)"
/lab_host="mixed (pool of 40 RNAs)"
/lab_host="mixed (pool of 40 RNAs)"
/lab_host="mixed (pool of 40 RNAs)"
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/clon
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NIH, Note: this is a NIH_MGC_Library."
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AGENCOURT_8907846 NIH_MGC_141 Homo saplens CDNA clone IMAGE:6388687
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 349)
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Tissue Procurement: NCI
CDNA Library Preparation: Michael Brownstein Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information and
found through the I.M.A.G.E. Consortium/LINL at:
http://image.lnl.gov
Plate: LLCM2590 row: i column: 08
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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Plate: LLCM2851 row: m column:
High quality sequence stop: 337.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
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BU589755
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5'-AAGCAGTGGGTCAACGCAATACGCCGGG-3' and 5'-AAGCAGTGGCCGACATG-CGGTG-3' and 5'-ARTCTAGAGGCCGACATG-GTG-10)NN-3'. Full-length enriched library was constructed using the Clontech creator SAMRY kit and size-selected to contain the 0.2-0.5 kb size fraction (other fractions present in NIH MGC.142). Library created in the laboratory of M. Brownstein (NIMH, NIH). Note: this is a NIH MGC Library."
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                                                                                                                                                                                                                                                                      //Clone_lib=_MXH_MCC_141"
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//Clone_lib=_MXH_M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                731 CAGGACAACTGGTCGTTACCAGACACCTATAACGTGTCCTCATCAATAATGTGTAAAACA 790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  289 GIGICGIGGAACCICITACIGCITICAAIACAGGAITAGIAAICNNNAAAAAAAAAAAAAA 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       791 GAAATAATCGATAGAATATTGAAAATAAATGTTAATAAACACTGGTTGAAATATGAAAA 850
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 438)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                   /clone="IMAGE:6603022"
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Pred. No. 1.3e+03;
0; Mismatches 95;
                                                             /organism="Homo sapiens"
/mol_type="mRNA"
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cDNA Library Preparation:
Location/Qualifiers
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51.8%;
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Homo sapiens
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                                           source
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ORIGIN
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KEYWORDS
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       FEATURES
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                                                                                                                                                                                                /clone="IMAGE:5388887"
/tissue_type="mixed (pool of 40 RNAs)".
/tab_host="Dation" (T1-phage resistant)"
/clone_lib="NHE_MGC_L11"
/clone_lib="NHE_MGC_L11"
/note="Vector: pDNR_LIB; Site_1: Sfil (ggccattatggcc);
Site_2: Sfil (ggccgctcggcc); Double-stranded cDNR was prepared from a pool of 40 cell line polyA+ RNAs (bladder - 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon - 4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%, kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary gland - 1.3%, and skin - 2.3%, prostate - 4.3%, salivary gland in cloning as follows:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5'-AACCAGTGGTFNTCAACGCGACATGGCCATTACGGCCGGG-3' and 5'-AACCAGTGGTFNTCAACGCCGACATG-dT(30)NN-3'. Full-length enriched library was constructed using the Clontech Creator SAMET kit and size-selected to contain the 0.2-0.5 kb size fraction (other fractions present in NIH_MGC_142). Library created in the laboratory of M. Brownstein (NIMH, NIH). Note: this is a NIH_MGC_Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             704 GTAGATCTATCAGACTACTTTTATCAGCAGGACAACTGGTCGTTACCAGACACCTATAAC 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        764 GIGICCICAICAATAAIGIGIAAAACAGAAAIAAICGAIAGAAIAIIGAAAAIAAAAIGI 823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 430)

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Tissue Procurement: NCI
CONN Library Preparation: Michael Brownstein Laboratory
CONN Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
thtp://image.llnl.gov
http://image.llnl.gov c column: 22
High quality sequence stop: 429.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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AGENCOURT_10402855 NIH_MGC_141 Homo sapiens cDNA clone
IMAGE:6603022 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 349;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             271 BABABABABABABABGGABABABABABABABABABA 311
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Pred. No. 1.5e+03;
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                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
   ity sequence stop: 332.
Location/Qualifiers
                                                                                                                                                                              /db_xref="taxon:9606"
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Homo sapiens
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       High quality
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                                        FEATURES
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830 ACACTGGTTGAAATATGAAAAAAAAAAAAAAAA 864
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                                                                                                                                                                                                                                                                     718 CTACTTTTATCAGCAGGACAACTGGTCGTTACCAGACACCTATAACGTGTCCTCATCAAT 777
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  778 AATGTGTAAAACAGAAATAATCGATAGAATATTGAAAATAATAATGTTAATAAACACTGGT 837
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Saccharomycetales; Saccharomycetaceae; Kluyveromyces.

I (bases 1 to 1068. M., Artiguenave,F., Blandin,G.,
Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S.,
de-Montigny,J., Dujon,B., Durrans,P., Lepingle,A., Liorente,B.,
Malpertuy,A., Neweglise,C., Caier-Kalogeropoulos,O., Potier,S.,
Saurin,W., Tekaia,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genomic exploration of the hemiascomycetous yeasts: 1. A set of
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Bolotin-Fuckuhara, M., Toffano-Nioche, C., Artiguenave, F.,

Duchateau-Nguyen, G., Lemaire, M., Marmeisse, R., Montrocher, R.,

Robert, C., Termier, M., Winoker, P. and Wesolowski-Louvel, M.

Genomic exploration of the hemiascomycetous yeasts: 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                           /tissue_type="posterior rhombomeres 5-8 (4 pooled)"
/dev_stage="embryo, 4 weeks postconception"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 5.4%; Score 47.4; DB 14; Length 438; Best Local Similarity 57.1%; Pred. No. 1.3e+03; Matches 84; Conservative 0; Mismatches 63; Indels 0
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      yeast species for molecular evolution studies
FEBS Lett. 487 (1), 3-12 (2000)
               info@image.llnl.gov
Plate: LLAM12412 row: B column: 24
Seg primer: MJRP1 reverse primer (ABI).
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5608631"
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FEBS Lett. 487 (1), 66-70 (2000)
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Genoscope.

Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
Direct Submission

Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail:
seqréfégenoscope.cns.fr - Web : www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces bayanus var. excharomyces
cataromyces kuyveromyces harmonices thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
angusta, Debaryomyces harmonia lipolytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Kluyveromyces lactis"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic DNA" /strain="CLIB 210"
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/clone="BA0AB030C03"
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3 (bases 1 to 1065)
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